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OM protein - protein search, using sw model

Run on: July 25, 2003, 11:38:01 ; Search time 84 Seconds
(without alignments)
610.341 Million cell updates/sec

Title: US-09-992-430B-22

Perfect score: 1625

Sequence: 1 MFQDTKSAQVTRDAKTQKV.....ELMEKSAQIKSVIEHLEIN 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 .

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1614.5	99.4	324	AAE25510	Kluyveromyces ther
2	952.5	58.6	313	AAE25511	Torulaspora pretor
3	663	40.8	319	AAE23265	Bacillus strain LN
4	654	40.2	319	AAE10591	L-lactic acid dehy
5	635	39.1	322	AAE2159	S. epidermidis ope
6	635	39.1	322	AAE2645	S. epidermidis ope
7	635	39.1	330	ABP39483	Staphylococcus epi
8	627	38.6	314	ABBS3683	Lactococcus lactis
9	622.5	38.3	314	AAE25997	B. flavum lactate

10	622.5	38.3	314	22	AAG2956	C glutamicum prote
11	622.5	38.3	314	22	ABY79307	Corynebacterium gl
12	617	38.0	313	23	ABY47671	Listeria monocytog
13	599	36.9	316	20	AAV20054	B. burgdorferi ant
14	596	36.7	327	23	ABR27743	Streptococcus poly
15	594.5	36.6	298	11	AAK08355	Recombinant thermo
16	594.5	36.6	298	11	AAK09295	Recombinant thermo
17	594	36.6	332	22	ABR64908	Drosophila melanog
18	589.5	36.3	325	23	ABBS4670	Lactococcus lactis
19	576.5	35.5	328	12	ABR15736	L-lactic acid dehy
20	576.5	35.5	328	24	ABU01649	S. pneumoniae type
21	576.5	35.5	332	24	ABP81596	Streptococcus pneu
22	576	35.4	329	23	ABP27742	Streptococcus poly
23	573	35.3	332	9	AAE08091	Testis-specific la
24	568	35.0	353	21	AAG30183	Arabidopsis thalia
25	562	34.6	332	22	AAW40272	Human polypeptide
26	562	34.6	332	23	ABF65331	Hypoxia-regulated
27	562	34.6	372	22	AAW42058	Human polypeptide
28	550.5	33.9	381	22	AAG89135	Human secreted pro
29	550.5	33.9	381	23	ABG32424	Human secreted pro
30	550.5	33.9	381	23	AAU11432	Human testicular l
31	548.5	33.8	295	20	AAV20055	B. burgdorferi ant
32	546	33.6	334	24	ABR47513	Breast cancer asso
33	546	33.6	334	24	ABU57627	Differentially exp
34	546	33.6	334	24	ABU07467	Protein differenti
35	546	33.6	354	22	ABG20193	Novel human diagno
36	546	33.6	354	22	ABG21596	Novel human diagno
37	545	33.5	333	18	AAW33108	Chicken lactic aci
38	543	33.4	333	23	ABG32957	Chicken lactate de
39	543	33.4	333	23	ABG32958	Chicken lactate de
40	542	33.4	327	23	ABP66043	Bifidobacterium lo
41	542	33.4	333	18	AAW33107	Chicken lactic aci
42	542	33.4	333	23	ABG32959	Chicken lactate de
43	542	33.4	338	22	AAU49896	Propionibacterium
44	535	32.9	333	10	AAE91948	Fig H4 isoenzyme
45	526	32.4	301	21	AAG30184	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAE25510

ID AAE25510 standard; Protein; 324 AA.

XX

AC AAE25510;

XX

DT 30-OCT-2002 (first entry)

XX

XX Kluyveromyces thermotolerans lactate dehydrogenase.

XX

Lactate dehydrogenase; lactic acid; fermentation; organic product;
food preservative; pharmaceutical product; cosmetic product; LDH;

XX

OS Kluyveromyces thermotolerans.

XX

PH Key Location/Qualifiers

FT Misc-difference 189

FT /note= "This residue is absent in the sequence

shown as SEQ ID NO:22 in sequence listing"

XX

PN WO200242471-A2.

XX

PD 30-MAY-2002.

XX

XX 23-NOV-2001; 2001WO-US44041.

XX

PR L-lactic acid dehy

XX

PR S. epidermidis ope

XX

XX (CRGI) CARGILL DOW POLYMERS LLC.

XX

PI Rajgarhia V;

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XX WPI; 2002-537387/57.
DR N-PSDB; AAD41577.
XX
XX New nucleic acid molecule encoding yeast lactate dehydrogenase protein
PT useful for transforming yeast cells for producing lactic acid
XX
XX Claim 1; Page 69-71; 157pp; English.
XX
XX The invention relates to nucleic acid molecules encoding yeast lactate
CC dehydrogenase (LDH) protein, especially Kluyveromyces thermotolerans or
CC Torulaspora pretoriensis LDH protein. Polynucleotides of the invention
CC are useful for transforming yeast cells for producing lactic acid by
CC fermentation. They are used for producing organic products e.g. esters,
CC carboxylates, carbohydrates, alditols, aldehydes, lactones, vitamins,
CC alkenes, alkyne, lipids, amino acids which are useful as preservatives
CC or additives in food, pharmaceutical or cosmetic products. They are
CC also used to make plastic and other products. The present sequence is
CC Kluyveromyces thermotolerans LDH protein.
XX
SQ Sequence 324 AA;

Query Match 99.4%; Score 1614.5; DB 23; Length 324;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 323; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MFQDTKSOAVRTDAKTAVVGVGSGSATAYTLILSGIVSEIVLIDVNDKKAEGESMD 60
DB 1 MFQDTKSOAVRTDAKTAVVGVGSGSATAYTLILSGIVSEIVLIDVNDKKAEGESMD 60
QY 61 LNHAAPSNTSRAGDYPDCAGAAIVITCGINQKNGQTRMDLAANKNANIMLEIIPNVAKY 120
DB 61 LNHAAPSNTSRAGDYPDCAGAAIVITCGINQKNGQTRMDLAANKNANIMLEIIPNVAKY 120
QY 121 APDTILLIATNPVDLTIYSKASGFPPLSRVIGSGTGLDTRFKYILGEHFKISSDSIDA 180
DB 121 APDTILLIATNPVDLTIYSKASGFPPLSRVIGSGTGLDTRFKYILGEHFKISSDSIDA 180
QY 181 CVIGEHGD-GVPMWLSLTNDGKRLDYCEKANHFIDQNAFHRIFEQTRDAAYDIIRKGY 239
DB 181 CVIGEHGDSGVPMWLSLTNDGKRLDYCEKANHFIDQNAFHRIFEQTRDAAYDIIRKGY 240
QY 240 TSYGIAAGLLRIVKAILEDTGSTLTSTVGVGDFGVEQIAISVPTKLNKSGAHQVAELSLD 299
DB 241 TSYGIAAGLLRIVKAILEDTGSTLTSTVGVGDFGVEQIAISVPTKLNKSGAHQVAELSLD 300
QY 300 EKEIEMKESASQIKSVIEHLEIN 323
DB 301 EKEIEMKESASQIKSVIEHLEIN 324

RESULT 2
AAE25511
ID AAE25511 standard; Protein; 313 AA.
XX
XX AAE25511;
XX
XX 30-OCT-2002 (first entry)
XX
XX Torulaspora pretoriensis lactate dehydrogenase.
XX
XX Lactate dehydrogenase; lactic acid; fermentation; organic product;
KW food preservative; pharmaceutical product; cosmetic product; LDH;
KW food additive; plastic product.
XX
XX Torulaspora pretoriensis.
OS
XX WO200242471-A2.
XX
XX 30-MAY-2002.
XX
XX 23-NOV-2001; 2001WO-US44041.
XX

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PR 22-NOV-2000; 2000US-252541P.
XX
XX (CRGI ) CARGILL DOW POLYMERS LLC.
XX
XX Rajgarhia V;
XX
XX WPI; 2002-537387/57.
DR N-PSDB; AAD41584.
XX
XX New nucleic acid molecule encoding yeast lactate dehydrogenase protein
PT useful for transforming yeast cells for producing lactic acid
XX
XX Claim 2; Page 144-146; 157pp; English.
XX
XX The invention relates to nucleic acid molecules encoding yeast lactate
CC dehydrogenase (LDH) protein, especially Kluyveromyces thermotolerans or
CC Torulaspora pretoriensis LDH protein. Polynucleotides of the invention
CC are useful for transforming yeast cells for producing lactic acid by
CC fermentation. They are used for producing organic products e.g. esters,
CC carboxylates, carbohydrates, alditols, aldehydes, lactones, vitamins,
CC alkenes, alkyne, lipids, amino acids which are useful as preservatives
CC or additives in food, pharmaceutical or cosmetic products. They are
CC also used to make plastic and other products. The present sequence is
CC Torulaspora pretoriensis LDH protein.
XX
SQ Sequence 313 AA;

Query Match 58.6%; Score 952.5; DB 23; Length 313;
Best Local Similarity 60.1%; Pred. No. 1.8e-80;
Matches 187; Conservative 55; Mismatches 66; Indels 3; Gaps 2;

QY 15 KTVKVVVGVGSGSATAYTLILSGIVSEIVLIDVNDKKAEGESMDLNHAAPSNTSR-- 72
DB 3 RCXKVAIVGAGQVSGTAYTLILSSVAEVLIDVDRKRVGGQFMDLNHAAPLTKESTRFS 62
QY 73 AGDYPDCAGAAIVITCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDTILLIATNP 132
DB 63 AGDYESCADAIVITCGANQKPGQTRMELAEKNVIMQEVIPKIVKYPANAILLIATNP 122
QY 133 VDVLTIYSKASGFPPLSRVIGSGTGLDTRFKYILGEHFKISSDSIDACVIGEHGD-GVP 191
DB 123 VDVLTIYSKASGFPASRVIGSGTGLDTRFKYILGEHFKISSDSIDACVIGEHGDSVP 182
QY 192 VWSLTNTDGMKRLDYCEKANHFIDQNAFHRIFEQTRDAAYDIIRKGYTSYGVIAAGLLRI 251
DB 183 VWSLAEIAGMKVEDYCEQSKRKFDPSPILTKIYESRDAAYIIRKGYTFTFGIAAGLLRI 242
QY 252 VKAILEDTGSTLTSTVGVGDFGVEQIAISVPTKLNKSGAHQVAELSDEKEIEMKESAS 311
DB 243 VRAILRDEGALLTVSTVGEHFGMKVDVSLVPTVRDPSGAAHVVDLLNDKLEQIKTSGA 302
QY 312 QIKSVIEHLEI 322
DB 303 KIKSACDELGI 313

RESULT 3
AAE23265
ID AAE23265 standard; Protein; 319 AA.
XX
XX AAE23265;
XX
XX 27-AUG-2002 (first entry)
XX
XX Bacillus strain LN lactate dehydrogenase (LDH).
XX
XX Thermophilic; recombination; gene mutation; ethanol production;
KW bacterial fermentation; lactate dehydrogenase; LDH; enzyme.
XX
XX Bacillus sp. TN.
OS
XX WO200229030-A2.
XX

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PD 11-APR-2002.
 XX 05-OCT-2001; 2001WO-GB04434.
 PF 06-OCT-2000; 2000GB-0024554.
 PR 13-NOV-2000; 2000US-247017P.
 XX (ELSW-) ELSWORTH BIOTECHNOLOGY LTD.
 FA Javed M, Cuesdin F, Milner P, Green E;
 FI WPI; 2002-426110/45.
 XX N-PSDB; AAD37417.
 DR Novel thermophilic gram-positive bacterium which has been transformed
 PT by homologous recombination for stabilizing a gene mutation and for
 PT inserting an expressible gene, useful for ethanol production -
 XX Claim 26; Fig 6; 44pp; English.
 XX The invention relates to a thermophilic gram-positive bacterium which
 CC has been transformed using a method of homologous recombination for
 CC stabilising a gene mutation and for inserting an expressible gene.
 CC The thermophilic gram positive bacterium is useful for continuous
 CC production of ethanol by bacterial fermentation, using optimised
 CC fermentation conditions, where the pH of the fermentation medium is
 CC within the range of pH 5.5-7.5, preferably 6.4-6.9, the temperature of
 CC the fermentation medium is within the range 40-75 degrees, preferably
 CC 60-68 degrees, and the feed dilution rate is 0.3-0.8 per hour, preferably
 CC 0.4-0.6 per hour. The method involves using air sparging within the
 CC culture such that the redox potential is between -360 to -400 mV,
 CC preferably 370 to -380 mV. The present sequence is Bacillus strain LN
 CC lactate dehydrogenase (LDH).
 XX SQ Sequence 319 AA;
 Query Match 40.8%; Score 663; DB 23; Length 319;
 Best Local Similarity 44.6%; Pred. No. 2.1e-53;
 Matches 136; Conservative 59; Mismatches 104; Indels 6; Gaps 4;
 QY 18 KVVVGVSGSATYATLLSGIVSEIVLIDVKNKKAEGESMDLNHA---APSNTRSRAG 74
 DB 8 RVALIGTFVGASAFALMNGQIADELVLIDVKNKKAEGDVMDLNKGKVPAPKPMNIWFG 67
 QY 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDTILLIATNPVD 134
 DB 68 DYQCDQADLVVICAGANQKPGETRLDLVDKNINIFKTIIVDSVMKSGFDGVFLVATNPVD 127
 QY 135 VLTIVSYKASGFPILSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
 DB 128 ILTYATWKFGLPKERVIGSGTILDTARFRLSEYFOVAPTNNHAYIIIEGHGDTPLPVW 187
 QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIEFTQTRDAAYDIIKRGYTSYGIAAGLLRIVK 253
 DB 188 SHAEIGSPVIEQILMQ-NDNRYRKEDLDNIFVNVDRDAAYQIIIEKKGATYGIAMGLVRI 246
 QY 254 AILEDGTSTLTVST-VGDFYFVEQIATSVPTKLNKSGAHQVAELSLDEKEIEMKESASQ 312
 DB 247 AILHNENAILTVSAHLDCQYGERNVYICVPAINNGIREVMELKLNTEQEQPHHSVTV 306
 QY 313 IKSVI 317
 DB 307 LKDIL 311
 RESULT 4
 AAR10591
 ID AAR10591 standard; Protein; 319 AA.
 AC AAR10591;
 XX 25-MAR-2003 (updated)
 DT 20-MAR-1991 (first entry)

XX L-lactic acid dehydrogenase.
 DE LDH; L-lactic acid; thermophile.
 XX LDH; L-lactic acid; thermophile.
 OS Bacillus strain TP-262.
 XX JF02286077-A.
 XX 26-NOV-1990.
 PD 27-APR-1989; 89JP-0108432.
 PF 27-APR-1989; 89JP-0108432.
 PR 27-APR-1989; 89JP-0108432.
 PA (TOYA) TOYAMA CHEM CO LTD.
 XX WPI; 1991-012213/02.
 DR N-PSDB; AAQ10162.
 XX Bacillus sp. pref. TP-262 stain - is thermophilic bacterium
 PT producing L-lactic acid dehydrogenase.
 PS Disclosure; Fig 1; 16pp; Japanese.
 XX The sequence was deduced from DNA which can be used to produce
 CC L-LDH by recombinant DNA techniques. The bacillus species contg.
 CC the DNA and able to express it is new and is thermophilic, growing
 CC at 50-70 deg.C.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 319 AA;
 Query Match 40.2%; Score 654; DB 12; Length 319;
 Best Local Similarity 43.9%; Pred. No. 1.5e-52;
 Matches 134; Conservative 59; Mismatches 106; Indels 6; Gaps 4;
 QY 18 KVVVGVSGSATYATLLSGIVSEIVLIDVKNKKAEGESMDLNHA---APSNTRSRAG 74
 DB 8 RVALIGTFVGASAFALMNGQIADELVLIDVKNKKAEGDVMDLNKGKVPAPKPMNIWFG 67
 QY 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDTILLIATNPVD 134
 DB 68 DYQCDQADLVVICAGANQKPGETRLDLVDKNINIFKTIIVDSVMKSGFDGVFLVATNPVD 127
 QY 135 VLTIVSYKASGFPILSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
 DB 128 ILTYATWKFGLPKERVIGSGTILDTARFRLSEYFOVAPTNNHAYIIIEGHGDTPLPVW 187
 QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIEFTQTRDAAYDIIKRGYTSYGIAAGLLRIVK 253
 DB 188 SHAEIGSPVIEQILSQ-NDNRYRKEDLDNIFVNVDRDAAYQIIIEKKGATYGIAMGLVRI 246
 QY 254 AILEDGTSTLTVSTVD-YFVEQIATSVPTKLNKSGAHQVAELSLDEKEIEMKESASQ 312
 DB 247 AILHNENAILTVSAYLDGQYNEQNVYICVPAINNGIREVMELKLNTEQEQPHHSVTV 306
 QY 313 IKSVI 317
 DB 307 LKDIL 311
 RESULT 5
 AAG82159
 ID AAG82159 standard; Protein; 322 AA.
 XX AAG82159;
 AC AAG82159;
 DT 03-SEP-2001 (first entry)
 XX S. epidermidis open reading frame protein sequence SEQ ID NO:1412.
 DE Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW

Query Match	38.6%	Score 627;	DB 23;	Length 314;
Best Local Similarity	43.9%	Pred. No. 4.8e-50;		
Matches 136; Conservative	59;	Mismatches 107;	Indels 8;	Gaps 5;

QY 18 KVVVGVGSGSATAYTLLLSGIYSEIVLIDVNVKDKAEGESMDLNHA---APSNTRSRAG 74
 Db 7 KVVVIGTGFVGTSAIYSGMINQGLVNLVLIDVNVQDKAEGEALDLDGVSQGENVIIVRAG 66
 QY 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
 Db 67 DYKCKNADIIVVTAGVNVKQSGRLDLVNTNAKIMRSIVTQWDSGDFGIFVIAASNPVD 126
 QY 135 VLTYSIKASGFPISRVISGTVLDTARPKYILGEHFKISSDSIDACVIGEHGDG-VPVW 193
 Db 127 ILTVVAVETSGLDQSRIVGTGTLDTTRFKELATKLEIDPRSVHGYIIGEHGDSEVAVW 186
 QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEQTRDAAYDIIRKGYTSYGTAAAGLLRIVK 253
 Db 187 SHTTVGGKRPILFEIVKNNKIGVED--LSNLSNKKVNAAYEIIDKQATYIGIGMSTARIVK 245
 QY 254 AILEDGTGTLTVSTV--GDYFGVEQIAISVPTKLNKSGAHQVAELSILDEKEIELMEKSAS 311
 Db 246 AILNNEQAILPVSAVLRGEY--GQGVFTGVPSIVNONGVREIILNIDAYEKKQFEKSVS 304
 QY 312 QIKSVIEHLE 321
 Db 305 QLKEVIESIK 314
 RESULT 9
 AAY25997
 ID AAY25997 standard; Protein; 314 AA.
 AC AAY25997;
 DT 18-OCT-1999 (first entry)
 DE B. flavum lactate dehydrogenase protein.
 KW Lactate dehydrogenase; destruction; lactic acid.
 XX Brevibacterium flavum.
 XX JP11206385-A.
 XX 03-AUG-1999.
 XX 28-JAN-1998; 98JP-0030594.
 XX 28-JAN-1998; 98JP-0030594.
 XX (MITU) MITSUBISHI CHEM CORP.
 XX WPI; 1999-486360/41.
 XX N-PSDB; AAZ09139.
 XX New lactate dehydrogenase gene and strain destroying gene - useful
 XX for formation of lactic acid
 XX Claim 1; Page 11-12; 13pp; Japanese.
 XX This invention describes the isolation of a novel lactate dehydrogenase
 XX protein from Brevibacterium flavum strain MJ-233. The invention also
 XX describes a microbial strain destroying the lactate dehydrogenase gene of
 XX a microbe in which the lactate dehydrogenase gene is destroyed by a
 XX homologous recombination of the above DNA or the above recombinant vector
 XX DNA with the lactate dehydrogenase gene on the chromosome DNA of the
 XX microbe cell and a method for the preparation of an amino acid or an
 XX organic acid in which the above strain destroying the lactate
 XX dehydrogenase gene is cultured in a medium and the amino acid or the
 XX organic acid (except lactic acid) is collected from the culture.
 XX Formation of lactic acid in the preparation of an amino acid and an
 XX organic acid can be decreased with no control of oxygen concentration
 XX during culture. This sequence represents the lactate dehydrogenase
 XX protein described in the specification.

SQ Sequence 314 AA;
 Query Match 38.3%; Score 622.5; DB 20; Length 314;
 Best Local Similarity 43.9%; Pred. No. 1.3e-49;
 Matches 134; Conservative 54; Mismatches 108; Indels 9; Gaps 5;
 QY 18 KVVVGVGSGSATAYTLLLSGIYSEIVLIDVNVKDKAEGESMDLNHA---APSNTRSRAG 74
 Db 8 KVLIGAGDVGVAYAYALINQGMADHLAIIIDIEKLEGNVMDLNGVWADSRTRVTKG 67
 QY 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
 Db 68 TYADCEAAWVVICAGAAQKPGETRLQLVDKVKIMKSIIVGDVWASGDFGIFVIAASNPVD 127
 QY 135 VLTYSIKASGFPISRVISGTVLDTARPKYILGEHFKISSDSIDACVIGEHGDG-VPVW 193
 Db 128 ILTVVAVETSGLEWNRVIGSGTVLDSARFYMIGELYEVAPSVHAYIIGEHGDTLPVL 187
 QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEQTRDAAYDIIRKGYTSYGTAAAGLLRIVK 253
 Db 188 SSATIAGVSLSRMLDKDPEL--EGRLEKIFEDTRDAAYHIIIDAKGSTSYGIGMLARITR 245
 QY 254 AILEDGTGTLTVSTV--GDYFGVEQIAISVPTKLNKSGAHQVAELSILDEKEIELMEKSAS 311
 Db 246 AILNQDVAVPVSAALLHGEY--GEEDIYIGTFVAVVNRGIRRVVLEITTDHEMERFKHSAN 304
 QY 312 QIKSV 316
 Db 305 TLREI 309
 RESULT 10
 AAG29956
 ID AAG29956 standard; Protein; 314 AA.
 AC AAG29956;
 DT 26-SEP-2001 (first entry)
 DE C glutamicum protein fragment SEQ ID NO: 6710.
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX Corynebacterium glutamicum.
 XX EF1108790-A2.
 XX 20-JUN-2001.
 XX 18-DEC-2000; 2000EP-0127688.
 XX 16-DEC-1999; 99JP-0377484.
 XX 07-APR-2000; 2000JP-0159162.
 XX 03-AUG-2000; 2000JP-0280988.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40..
 XX N-PSDB; AAH68175.
 XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 XX mutation point of a gene, measuring expression of a gene, analysing
 XX expression profile or pattern of a gene and identifying homologous gene
 XX Claim 17; SEQ ID NO: 6710; 246pp + Sequence Listing; English.
 XX The present invention provides a number of nucleotide and protein
 XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These

are useful for identifying the mutation point of a gene derived from a mutant of *Corynebacterium*, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from *Corynebacterium*, and identifying a homologue of a gene derived from *Corynebacterium*. *Corynebacterium* bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.

AA	Sequence	314 AA;
SQ		

Query Match	38.3%;	Score	622.5;	DB	22;	Length	314;
Best Local Similarity	43.9%;	Pred. No.	1.3e-49;				
Matches	134;	Conservative	54;	Mismatches	108;	Indels	9;
Gaps	5;						
QY	18	KVVVGVGVSGVSATAYTLLLSGVISEVLVDVKNKAEGESMDLNHA--APNTRSRAG	74				
DB	8	KIVLIGAGDVGVAYVALINQGWADHAIIDIDKLEGNVMDLNHGVMWADSRKTRVTKG	67				
QY	75	DYDPCAGAAIVIVTCGINQKNGQTRMDLAAKNANIMLEIIPNVAKYAPDTILLIATNPVD	134				
DB	68	TYADCEDAANVICAGAAQKPGETRLQVQNVKIMKSIIVGDVWDSGDFGIFLVASNPVD	127				
QY	135	VLTYISYKASGFPPLSRVIGSGTVLDTARFYIIGEHPKISDSDIDACVIGEHD-GVPVW	193				
DB	128	ILTYAVWKFSGLEWNRVIGSGTVLDSARFYMGLGELYEVAQSSVHVAVIIEGHGDTLPVL	187				
QY	194	SLTNIDGMKLRDCEKANHIFDQNAFHRIEFQTRDAAYDIIKRGVTSYIGIAGLLIRIVK	253				
DB	188	SSATIAGVLSRMLDKDQPEYL--EGRLKEFIEDTRDAAYHIIIDAKGSTSYGIGMGLARITR	245				
QY	254	AILEDGTGSTITVSTV--GDYFVGVEQAIISVPTKLKNSGAHVAELSDEKEIFELMEKSA	311				
DB	246	AIIQNQDVAVPVSAIIHGEY-GEEDIYIGTPAVVNRGIRRVVELEITDHEMERFKHSAN	304				
QY	312	QIKSV	316				
DB	305	TLREI	309				

RESULT 11
AAB79307
ID AAB79307 standard; Protein; 314 AA.

AC AAB79307;

DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum SMP protein sequence SEO ID NO:130.

Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; carbonyls; Corynebacterium diphtheriae; evolutionary study.

OS *Corynebacterium glutamicum*.

PN WO200100844-A2.

04-JAN-2001.

23-JUN-2000: 2000WO-IB00943.

25-JUN-1999: 99US-0141031

PK 08-JUL-1999; 99DE-1031412.
PR 08-JUL-1999; 99DE-1031413.

PK 08-JUL-1999; 99DE-1031419.

PR	08-JUL-1999;	99DE-1031420.
PR	08-JUL-1999;	99DE-1031424.
PR	08-JUL-1999;	99DE-1031428.
PR	08-JUL-1999;	99DE-1031431.
PR	08-JUL-1999;	99DE-1031433.
PR	08-JUL-1999;	99DE-1031434.
PR	08-JUL-1999;	99DE-1031510.
PR	08-JUL-1999;	99DE-1031562.
PR	08-JUL-1999;	99DE-1031634.
PR	09-JUL-1999;	99DE-1032180.
PR	09-JUL-1999;	99DE-1032227.
PR	09-JUL-1999;	99DE-1032320.
PR	09-JUL-1999;	99US-0143208.
PR	14-JUL-1999;	99DE-1032924.
PR	14-JUL-1999;	99DE-1032973.
PR	14-JUL-1999;	99DE-1033005.
PR	27-AUG-1999;	99DE-1040765.
PR	31-AUG-1999;	99US-0151572.
PR	03-SEP-1999;	99DE-1042076.
PR	03-SEP-1999;	99DE-1042079.
PR	03-SEP-1999;	99DE-1042086.
PR	03-SEP-1999;	99DE-1042088.
PR	03-SEP-1999;	99DE-1042095.
PR	03-SEP-1999;	99DE-1042123.
PR	03-SEP-1999;	99DE-1042125.

XX
PA (BADI) BASE AG.

PI Pompeius M. Kroeger B. Schroeder H. Zelder O. Haberhauer G:
XX

AA
DR WPI: 2001-061975/07.

UK N-PSDB; HAF / 1424;
XX

PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,
PT carbohydrates or enzymes -

PS Claim 20; Page 333-334; 1246pp; English.

CC AAF71360 to AAF717

CC AAB79243 to AAB 79633 which are involved in carbon metabolism

CC (II) for expression in host cells and production or modulation of energy production: the C: glutamicum SMF gene can be used in v

CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine production or line chemicals, such as, an organic acid, a protein

XX Key Location/Qualifiers
 FH Misc-difference 108..108
 FT /label=Ser or Thr
 FT Misc-difference 169..169
 FT /label=Ser or Thr
 XX
 PN WO9010702-A.
 XX
 PD 20-SEP-1990.
 XX
 PF 07-MAR-1990; 90WO-GB00345.
 XX
 PR 08-MAR-1989; 89GB-0005269.
 XX
 PA (PUBL-) PUBLIC HEALTH LAB S.
 PA (UYBR-) UNIV BRISTOL.
 XX
 PI Chia WN, Clarke AR, Holbrook JJ, Wilks HM, Atkinson A;
 XX WPI; 1990-305025/40.
 XX
 PT Recombinant thermophilic NAD-dependent dehydrogenase - having a
 PT hydrophobic amino acid at position 102 and/or 104 and/or a change
 PT at 234-237
 XX
 PS Disclosure; fig 1; 30pp; English.
 XX
 CC This recombinant thermophilic NAD-dependent dehydrogenase has a
 CC sequence with at least 75% homology with that of B.steartthermoph-
 CC ilus lactate dehydrogenase. The altered amino acids are at posns.
 CC 106-110 and 167-172. It has a higher catalytic activity for
 CC homologues of lactic acid of formula: C(n) H(2n + 1) COHCOOH,
 CC n= greater than 1, than for lactate as well as a higher catalytic
 CC activity for malate than for lactate. It can be used to convert a
 CC keto cpd. stereospecifically to a corresp. secondary alcohol.
 CC This prodn. of individual optical isomers (o.i.) is useful in the
 CC mfr. of o.i.'s of pharmaceuticals and drug intermediates.
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 Best Local Similarity 42.6%; Pred. No. 4.9e-47;
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 DB 68 DYDCRDADLVVICAGANQKPGETRLDLVDKKIAIFRSSEXRLMASGFGGLFLVATNPVD 127
 QY 135 VLTYSIKASGFPILSRVIGSGTGLDTRFKVILGEHFKISSDSIDACVIGEHGD-GVPVW 193
 DB 128 ILTVATKFSGLPHERVIGSGTGLDTRFKVILGEHFVSLDXARFAYIIGEHGDELVPVW 187
 QY 194 SLTNDGKMLRDYCEKANHIFDQNAFHRIPEQTRDAAYDIIRKGYTSYTAAGLLRIVK 253
 DB 188 S-----QAKD-----LERIFVNRDAAYQIIKKGATYGIAMGLARVTR 227
 QY 254 AILEDGTGTLTVSTVGD-YFGVEQIAISVPTKLNKSGAHQVAELSLDEKTELMKESASQ 312
 DB 228 ALLHENAALTVSAYDGLYGERDVYIGVPAVINNRNGIREVIEIELNDDKQNRPHHSAAT 287
 QY 313 IKSVI 317
 DB 288 LKSVL 292

Search completed: July 25, 2003, 11:43:44
 Job time : 86 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2003, 11:42:17 ; Search time 29 Seconds
(without alignments)
471.255 Million cell updates/sec

Title: US-09-992-430B-22

Perfect score: 1625

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	648	39.9	317	1	US-08-748-068-3
2	635	39.1	330	4	US-09-134-001C-4328
3	599	36.9	324	4	US-09-107-532A-6486
4	578	35.6	331	4	US-09-711-681-4
5	569.5	35.0	307	4	US-09-107-532A-4274
6	562.5	34.6	327	1	US-08-748-068-2
7	550.5	33.9	381	4	US-09-711-681-2
8	545	33.5	333	2	US-08-869-506-3
9	545	33.5	333	3	US-09-128-967-3
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12	535	32.9	333	1	US-08-748-068-1
13	492	30.3	320	3	US-09-535-381-2
14	425	26.2	329	1	US-08-270-013B-2
15	425	26.2	329	1	US-08-838-418-2
16	395	24.3	325	4	US-09-134-001C-5533
17	383	23.6	315	5	PCT-US94-03796-2
18	329	20.2	330	3	US-08-676-882-2
19	324	19.9	304	4	US-09-634-238-238
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22	178.5	11.0	338	3	US-08-922-957-1
23	164.5	10.1	298	3	US-08-922-957-4
24	151.5	9.3	95	4	US-09-724-623-108
25	143	8.8	273	4	US-09-091-097-12
26	134.5	8.3	327	1	US-08-211-682-25
27	103.5	6.4	453	1	US-08-374-155A-8

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Sequence 6037, Ap
Sequence 333, App
Sequence 105, App
Sequence 5781, Ap
Sequence 5280, Ap
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Sequence 268, App
Sequence 282, App
Sequence 266, App
Sequence 10, Appl
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Sequence 2, Appli

28 103.5 6.4 453 2 US-08-785-396-8
29 103 6.3 3892 4 US-09-328-352-5503
30 98.5 6.1 906 4 US-09-328-352-6037
31 97.5 6.0 474 4 US-08-311-731A-353
32 97.5 6.0 725 4 US-08-311-731A-105
33 97 6.0 684 4 US-09-328-352-5781
34 96 5.9 302 4 US-09-107-532A-5280
35 95.5 5.9 251 4 US-09-648-004-20
36 95 5.8 558 4 US-09-071-035-268
37 95 5.8 1638 4 US-09-071-035-258
38 95 5.8 1638 4 US-09-071-035-262
39 95 5.8 1638 4 US-09-071-035-266
40 94 5.8 509 4 US-09-499-302A-10
41 93.5 5.8 422 3 US-08-961-083-116
42 93.5 5.8 422 4 US-09-536-784-116
43 93 5.7 893 4 US-09-328-352-6626
44 92 5.7 267 4 US-09-773-748-1
45 91.5 5.6 444 4 US-08-940-572-2

ALIGNMENTS

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; Patent No. 5770410
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; APPLICANT: Chiral Synthesis
; TITLE OF INVENTION: Chiral Synthesis
; NUMBER OF SEQUENCES: 15
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BFO)
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; APPLICATION NUMBER: US/08/748,068
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,959
; FILING DATE: 05-OCT-1994
; APPLICATION NUMBER: GB 92 02033.8
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 04702.6
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 93/00204
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; LENGTH: 317 amino acids
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
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RESULT 2

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US-09-134-001C-4328
; Sequence 4328, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lyn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4328
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4328

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Query Match 39.1%; Score 635; DB 4; Length 330;
Best Local Similarity 43.1%; Pred. No. 1e-58;
Matches 137; Conservative 57; Mismatches 100; Indels 24; Gaps 6;

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Qy 75 DYPDCAGAAIVITCGINQNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
Dy 81 EYEDCKDADLVITAGAPQKPGETRLQVKNKIMKSVTSVWDGSGDFGLIATNPVD 140
Qy 135 VLTYSYKASGFPFLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHDG-GVPVW 193
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Qy 194 SLTNIDGMKLRDYCE-----KANHIFDQNAFHRIFEQTRDAAYDIIKEKGYTSVGI 246
Dy 201 SQANVGISVYDTLKEETGSDAKAN-----EIIYINTRDAAYDIIQAKGTYTYGIAL 251
Qy 247 GILIRVKAILEDGTLTIVST-VGDYFGEVQIAISVPTKLKSCAHQVAELSDKEIEL 305
Dy 252 ALLRISKALLNNENSILTVSSQLNGQYGFNDVYLGPLTLNQNGAVKIYETPLNDNELQL 311
Qy 306 MEKSASQIKSV-----IEHL 320
Dy 312 LEKSVKLTEDYDSIKHL 329

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RESULT 3

US-09-107-532A-6486
; Sequence 6486, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS: 7310
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6486:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
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; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...324
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US-09-107-532A-6486

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Qy 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDITILLIATNPVD 134
Db 77 GYEECKDADIVITAGINQKQSRDLQVKNASIMEQIVKEIMGSGFDGIIVVASNPVD 136
Qy 135 VLTIVSYKASGFPPLSRVIGSGTVLDTARFKYLGEHFKISDSIDACVIGEHGDG-VPVW 193
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Qy 194 SLTNIDGMKLRDCEKANHFIDQNAFHRIPEOTRDAAYDIIKRKYTSYGAAGLLRIVK 253
Db 197 SHTTVGKPVFEIVK-DHRIAQDELVDIAKVRNAAYEIIDRKKATYYGIGMSTARIVK 255

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Db 256 AILNNEQAVLPVSAYLTYGTY-DEKIDFTGVPSIVDENGVRVVELSINBEKAMPSKSTS 314
Qy 312 QIKSVI 317
Db 315 ALREVL 320

RESULT 4

US-09-711-681-4
; Sequence 4, Application US/09711681
; Patent No. 6503743
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al.
; TITLE OF INVENTION: Isolated Human Secreted Proteins,
; Nucleic Acid Molecules Encoding Human Secreted Proteins And
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: CLO00839
; CURRENT APPLICATION NUMBER: US/09/711,681
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-711-681-4

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Best Local Similarity 38.5%; Pred. No. 1.1e-52;
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Db 22 KITVGVGAVGMACALSIILMKDLADELALVDVNMEDKLKGMMDLQGLSLKPKIVSSK 81
Qy 73 AGDYPDCAGAAIVIVTCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDITILLIATNP 132
Db 82 --DYCVTANSKLVIITAGARQSGESRLNLVQRNVNIFKFIIPNVKYSPhCKLLIVSNP 139
Qy 133 VDVLTVSYKASGFPPLSRVIGSGTVLDTARFKYLGEHFKISDSIDACVIGEHGD-GVP 191
Db 140 VDILTYVAMKISGFPKPNRVIGSGCNLDSARFRLMGERLGVHLSCHGWVIGHGDSSVP 199
Qy 192 VWSLTNIDGMKLRDCEKANHFIDQNAFHRIPEOTRDAAYDIIKRKYTSYGAAGLLRI 251
Db 200 VMSGVNVAGVSLKSLNPELGTADKQWKEVHKQVDSAYEIVLKYTSWALGLSVADL 259
Qy 252 VKAILEDGTSTLTVST--VGDFYFGV-EQIAISVPTKLNKSGAHQVAELSLDEKEIELMK 309
Db 260 AESIMKNLRRVHPISITMKGILYINEDVFLSVPCILGQNGISDVVKVTLTPPEEARLKS 319
Qy 310 ASQIKSVIEHLE 321
Db 320 ADTLWGIQELQ 331

RESULT 5

US-09-107-532A-4274
; Sequence 4274, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA


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US-08-748-068-2

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Best Local Similarity 39.4%; Pred. No. 4.7e-51;
Matches 125; Conservative 67; Mismatches 116; Indels 9; Gaps 7;
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Qy 10 VRTDAKTVVVVGVSGVSATATLLSGIVSEIVLIDVNDKKAEGESMDLNHAAP--S 67
Db 12 IEDDESQKITVGTGAVGWACAISILLKDLADELALVDLKDKGEMDLQHSIFFS 71
Qy 68 NTRSRAG-DYPDCAGAAIVITCGINQNGQTRMDLAANKANIMLEIIPNVAKYADPTIL 126
Db 72 TSKVTSGKTSVANSRIVITAGARQGEETRLALVQRNVAIMKIIPAIHVSPDKI 131
Qy 127 LIATNPVDVLTYSYKASGPLSRVIGSGTGLTDAREKYILGHEHFKISSDIDACVIGEH 186
Db 132 LVVSNPVDILTIVWKSGLPVTGVGNCNLSARFRYLIGKLVGHPVTSCHGWIIEH 191
Qy 187 GD-GVPVWSLTNIDGMKLDYCEKANHFQDNAFHRIPEQTRDAAYDIIRKGYTSYGIA 245
Db 192 GDSSVPLWSGVNAGVALKTLDPKLGTDSDKEHWNKHQVIOISAYEIIKLKGYTSWAIG 251
Qy 246 AGLLRIVKALIEDTGSTLTSTV--VDYFGV--EQIAISVPTKLKSGAHQVAELSLDEKEI 303
Db 252 LSVMDLVP--LKNLRVHPVSTVWVTKGLYGIEKELFLSIPCVLGNVGVSVDVVKIDLSSEB- 308
Qy 304 ELMKASQIKSVIEHL 320
Db 309 ALLKSAETLWNQKNL 325
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RESULT 7
US-09-711-681-2
; Sequence 2, Application US/09711681
; Patent No. 6503743
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al.
; TITLE OF INVENTION: Isolated Human Secreted Proteins,
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Secreted Proteins And
; FILE REFERENCE: CL000839
; CURRENT APPLICATION NUMBER: US/09/711,681
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-711-681-2

Query Match 33.9%; Score 550.5; DB 4; Length 381;
Best Local Similarity 36.3%; Pred. No. 1.1e-49;
Matches 119; Conservative 76; Mismatches 122; Indels 11; Gaps 5;

Qy 6 KQAVR--TDKTV--KVVVGVSGVSATATLLSGIVSEIVLIDVNDKKAEGESMD 60
Db 54 KSELIERFTSEKPVHHSKVSIICTGSGVWACAISILLKGLSDELALVDLDEDLKGETMD 113
Qy 61 LNHAAPNTRSR---AGDYPDCAGAAIVITCGINQNGQTRMDLAANKANIMLEIIPNV 117
Db 114 LQHGSPFTKMPNIVCSKDYFVTANSNLVIITAGARQGEETRLNLVQRNVAIFKLMISSI 173
Qy 118 AKYAPDTILLIATNPVDVLTYSYKASGPLSRVIGSGTGLTDAREKYILGHEHFKISSDS 177
Db 174 VQSPHCKLIIVSNPVDILTIVAWKLSAFPKNRIISGNCNLDTARFRFLIGQKLGHSES 233
Qy 178 IDACVIGEHGD-GVPVWSLTNIDGMKLDYCEKANHFQDNAFHRIPEQTRDAAYDIIRK 236
Db 234 CHGMILGEHGDSSVPVWSGVNIAGVPLKOLNSDIGTDKPEQWKNVHKEVTATAYEIIKM 293
Qy 237 KGYTSYGIAGLLRIVKALIEDTGSTLTSTV--GDYFGVEQIAISVPTKLKSGAHQVA 294
Db 294 KGYTSWAIGLSVADLTESILKLNLRHPVSTITKGLYGIDEVFLSIPCVLGNVGITNLI 353
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Db 354 KIKLTPEEBAHLKKSATLWEIQNKLL 381
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RESULT 8
US-08-869-506-3
; Sequence 3, Application US/08869506
; Patent No. 5827710
; GENERAL INFORMATION:
; APPLICANT: Uchida, Kohji
; APPLICANT: Matsukawa, Hirokazu
; APPLICANT: Matuo, Yushi
; APPLICANT: Fujita, Teyosi
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: NIXON & VANDERHUYE P.C.
; STREET: 1100 No. 5827710th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,506
; FILING DATE: 05-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 73797/1996
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 159-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/869,506
; FILING DATE: 05-JUN-1997
; APPLICATION NUMBER: JP 73797/1996
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 159-43
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; QUERY MATCH 33.5%; Score 545; DB 3; Length 333;
; Best Local Similarity 36.8%; Pred. No. 3.4e-49;
; Matches 114; Conservative 71; Mismatches 119; Indels 6; Gaps 4;
QY 18 KVVVGVGSGSATAYTLLSIVSEIVLIDVNKDKAESGMDLNHAA---PSNTRSRAG 74
DB 22 KITVVGVGQGVMACAISILGKLCDLALVDLEDKLGEMMDLQHGSLFLQTHKIADK 81
QY 75 DYPDCAGAAIVTVTCGINQKNGOTRMDLAANKANIMLEIIIPNVAKYAPDTILLIATNPVD 134
DB 82 DVAVTANSKIVVTAGVRQEGESRLNVQRNVNFVKFIIPQIVKYSPNCVILVVSNPVD 141
QY 135 VLTYSYKASGPPLSERVIGSGTVLDTPARKYLGEHFHKISSDSIDACVIGEHGD-GVPVW 193
DB 142 ILTYVTWKLSGLPKHRVIGSGCNLDTPARFRYLMAERLGIHTPSTCHGWTLGSHGSSVAW 201
QY 194 SLTNIDGMKLRDCEKANHIIFQNAFHRIFFQTRDAAYDIIRKKGYSYGIAAGLLRVK 253
DB 202 SGNNVAGVSLQLDPAMGTDXSENKEVHQVVEAVEVIRLGYNTWAIGLSVAELCE 261
QY 254 AILEDGTSLTVST-VGDYFGVE-QIAISVPTKLNKSGAHQVAEISLDEKEIELMEKSAS 311
DB 262 TMLKNLYRVHSVSTLVKGTGYGIENDVFSLPCVLSASGLTSVINQKLKDDEVAQLKKSD 321
QY 312 QIKSVIEHLE 321
DB 322 TLWSIQOLK 331
RESULT 9
US-09-128-967-3
; Sequence 3, Application US/09128967
; Patent No. 6057141
; GENERAL INFORMATION:
; APPLICANT: Uchida, Kohji
; APPLICANT: Matsukawa, Hirokazu
; APPLICANT: Matuo, Yushi
; APPLICANT: Fujita, Tuyoosi
; TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN LACTATE DEHYDROGENASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 No. 6057141ch Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:

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;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
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;; APPLICATION NUMBER: US/08/748,068
;; FILING DATE: 12-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/256,959
;; FILING DATE: 05-OCT-1994
;; APPLICATION NUMBER: GB 92 02033.8
;; FILING DATE: 30-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 92 04702.6
;; FILING DATE: 04-MAR-1992
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;; APPLICATION NUMBER: GB 93/00204
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 333 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
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Best Local Similarity 35.3%; Pred. NO. 3.9e-48;
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DB 82 --DYSVTANSKIVVTVAGVRQEGESRLNLQVRNVNFKPIIPQIVKYSNCIIIVVSNP 139
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QY 192 VWSLTNIDGMKLRDCEKANHFIDQNAFHRIFQTRDAAYDIIRKGYTSYGAAGLRI 251
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QY 252 VKAILEDGTSTLTST-VGDYFGVE-QIAISVPTKLKSGAHQVABLSLDEKEIEMLEKS 309
DB 260 IESMLKNLSRIHPVSTVMQVGYIENEVFLSLPCVLNARGLTSVINQKLKDDVAQLKNS 319
QY 310 ASQIKSVIEHLE 321
DB 320 ADTLWGIQKDLK 331
RESULT 13
US-09-535-381-2
;; Sequence 2, Application US/09535381
;; Patent No. 6268189
;; GENERAL INFORMATION:
;; APPLICANT: Skory, Christopher D
;; TITLE OF INVENTION: Fungal Lactate Dehydrogenase Gene and Constructs for
;; TITLE OF INVENTION: the Expression Thereof
;; FILE REFERENCE: Dkt 0110.98 - Christopher D. Skory
;; CURRENT APPLICATION NUMBER: US/09/535,381
;; CURRENT FILING DATE: 2000-03-24
;; NUMBER OF SEQ ID NOS: 8
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; SEQUENCE CHARACTERISTICS:
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 ; MOLECULE TYPE: protein
 ; US-08-838-418-2

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Qy	68	NTRSRAGDYPDCAGAAIVIVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILL	127
Db	63	NIIG-TSDYADTADSDIIVITAGIARKPGMSRDDLVTTNQKIMQVTKVVKYSPNCYII	121
Qy	128	IATNPVDVLTYSISKASGFPPLSRVIGSGTVLDTARFKVILGEHFKISSDSIDACVIGEHG	187
Db	122	VLTPNPVDMTYTVFKESGFPKRVIGOSGVLDTARFRTFVAEELNISVKDVTGFLVGGHG	181
Qy	188	DG-VPVWSLTNIDGMKLRDYCEKANHIFDQNAFHRIFEQTRDAAYDIIKKKGYS--YGI	244
Db	182	DDWYPLVRYSYAGGIPL-----EK---LIPKRLDAIVERTEKGGGEIVNLLNGSAYYAP	234
Qy	245	AAGLLRIVKAILEDGTSL-TVSTVGDFYGVGEQIAISVPTKLNKSGAHQVAELSDEKE	302
Db	235	AASLVEMVEALKDQRRILPAIAYLEGEYGYEGYILGVPTILGGNGIEKVIETLELTEE	293

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-992-430B-22

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Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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3	622.5	38.3	314	10	Sequence 9, Appli
4	578	35.6	331	15	Sequence 6710, Ap
5	550.5	33.9	381	10	Sequence 4, Appli
6	550.5	33.9	381	15	Sequence 255, App
7	546	33.6	334	15	Sequence 2, Appli
8	546	33.6	334	15	Sequence 75, Appli
9	324	19.9	301	10	Sequence 262, App
10	280.5	17.3	148	10	Sequence 262, App
11	280.5	17.3	148	10	Sequence 215, App
12	280.5	17.3	148	15	Sequence 215, App
13	223.5	13.8	303	15	Sequence 215, App
14	202.5	12.5	146	15	Sequence 7888, Ap
15	186.5	11.5	142	9	Sequence 6816, Ap
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17	156.5	9.6	322	9	US-09-874-923-112	Sequence 112, App
18	156.5	9.6	322	10	US-09-991-496-112	Sequence 112, App
19	143	8.8	273	15	US-10-109-670-13	Sequence 13, Appli
20	140.5	8.6	139	10	US-09-731-872-256	Sequence 256, App
21	126	7.8	495	15	US-10-156-761-9861	Sequence 9861, Ap
22	117	7.2	81	11	US-09-764-891-3783	Sequence 3783, Ap
23	106	6.5	445	15	US-10-156-761-9293	Sequence 9293, Ap
24	103.5	6.4	453	15	US-10-061-269-8	Sequence 8, Appli
25	98	6.0	333	15	US-10-156-761-10268	Sequence 10268, A
26	98	6.0	494	15	US-10-006-852-4	Sequence 4, Appli
27	95.5	5.9	251	15	US-10-272-419-20	Sequence 20, Appli
28	94.5	5.8	564	15	US-10-156-761-10095	Sequence 10095, A
29	93.5	5.8	326	9	US-09-841-132-447	Sequence 447, App
30	93.5	5.8	422	9	US-09-765-272-116	Sequence 116, App
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34	91.5	5.6	329	15	US-10-156-761-10973	Sequence 10973, A
35	91.5	5.6	444	9	US-09-815-242-13507	Sequence 13507, A
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37	90	5.5	569	15	US-10-156-761-12273	Sequence 12273, A
38	90	5.5	1257	9	US-09-738-363-6	Sequence 6, Appli
39	89.5	5.5	385	9	US-09-815-242-11553	Sequence 11553, A
40	88.5	5.4	328	9	US-09-892-867-3	Sequence 3, Appli
41	88.5	5.4	328	10	US-09-738-626-6112	Sequence 6112, Ap
42	88	5.4	319	15	US-10-122-466A-14	Sequence 14, Appli
43	87	5.4	304	9	US-09-925-302-614	Sequence 614, App
44	87	5.4	580	15	US-10-156-761-12566	Sequence 12566, A
45	87	5.4	2092	15	US-10-128-714-3061	Sequence 3061, Ap

ALIGNMENTS

RESULT 1

US-09-971-361-3

; Sequence 3, Application US/09971361

; Patent No. US20020081677A1

; GENERAL INFORMATION:

; APPLICANT: Javed, Muhammad

; APPLICANT: Cusdin, Fiona

; APPLICANT: Milner, Paul

; APPLICANT: Green, Edward

; TITLE OF INVENTION: Ethanol Production

; FILE REFERENCE: 000487.00010

; CURRENT APPLICATION NUMBER: US/09/971,361

; CURRENT FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: US 60/247,017

; PRIOR FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: UK 0024554.8

; PRIOR FILING DATE: 2000-10-06

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 319

; TYPE: PRT

; ORGANISM: Bacillus LN

US-09-971-361-3

Query Match 40.8%; Score 663; DB 9; Length 319;

Best Local Similarity 44.6%; Pred. No. 8.2e-60;

Matches 136; Conservative 59; Mismatches 104; Indels 6; Gaps 4;

QY 18 KVVVGVGVGATATYLLSGIVSEIVLIDVNNKKAEGSDMLNFA---APNTRSRAG 74

Db 8 RVALIGTFVGASAFALNMQGIADLVLIDVNNKKAEGSDMLNFKGVFAPKPMNIWF 67

QY 75 DYPDCAGAAIVTVTCGINKGQTRMDLAANKANIMLEIIPNVKYPADPTILLIANTPVD 134

Db 68 DYQDCQDADLVICAGANQKPGTGLDLVDKNNINIFKTVDSVNNKSGFGVFLVATNPVD 127

QY 135 VLTYISYKASGFFLSRVIGSGTVLDTARPKYILGHEFKISSDSDIDACVIGEHGD-GVPVW 193

Db 128 ILTYATWFKSGLPKRVISGTLTDARFRLSEYFQVAPTNVHAYIIGEHGDTPLVW 187
Qy 194 SLTNIDGKMLRDYCEKANHIFDQNAFHRIEFTQTRDAAYDIIRKGYTSYGIAGLLRIVK 253
Db 188 SHAIEGSPVEQILMQ-NDNVRKEDLDNIFVNRDAAYQIIEKKGATYGIAMGLVRITR 246
Qy 254 AILEDGTLTSTVST-VGDYFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIEMKESASQ 312
Db 247 AILHNNAILTVSAHLDGQYGERNVYIGVPAIINRNGIREVMELTNETEQQQPHHSVTV 306
Qy 313 IKSVI 317
Db 307 LKDIL 311

RESULT 2

US-09-971-361-9
; Sequence 9, Application US/09971361
; Patent No. US20020081677A1
; GENERAL INFORMATION:
; APPLICANT: Javed, Muhammad
; APPLICANT: Cusdin, Fiona
; APPLICANT: Milner, Paul
; APPLICANT: Green, Edward
; TITLE OF INVENTION: Ethanol Production
; FILE REFERENCE: 000487.00010
; CURRENT APPLICATION NUMBER: US/09/971.361
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/247,017
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: UK 0024554.8
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Bacillus strain TN
US-09-971-361-9

Query Match 40.8%; Score 663; DB 9; Length 319;
Best Local Similarity 44.6%; Pred. No. 8.2e-60;
Matches 136; Conservative 59; Mismatches 104; Indels 6; Gaps 4;
Qy 18 KVVVGVGVSATAYTLLLSGIVSEIVLIDVKNKKAEGESMDLNHA---APSNTRSRAG 74
Db 8 RVALIGTGFGVASYAFALMNOGIADELVLIDVKNKKAEGDVMDLNHKGVPAPKPMNIWFG 67
Qy 75 DYPDCAGAAIVITCGINQKNGOTRMDLAANKNANIMLEIIPNVAKYAPDTILLIATNPVD 134
Db 68 DYQCDQADLVVICAGANQKPGETRLDLVDKNNIFKTVDSVMKSGDGVFLVATNPVD 127
Qy 135 VLTIVSYKASGFPPLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
Db 128 ILTYATWFKSGLPKRVISGTLTDARFRLSEYFQVAPTNVHAYIIGEHGDTPLVW 187
Qy 194 SLTNIDGKMLRDYCEKANHIFDQNAFHRIEFTQTRDAAYDIIRKGYTSYGIAGLLRIVK 253
Db 188 SHAIEGSPVEQILMQ-NDNVRKEDLDNIFVNRDAAYQIIEKKGATYGIAMGLVRITR 246
Qy 254 AILEDGTLTSTVST-VGDYFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIEMKESASQ 312
Db 247 AILHNNAILTVSAHLDGQYGERNVYIGVPAIINRNGIREVMELTNETEQQQPHHSVTV 306
Qy 313 IKSVI 317
Db 307 LKDIL 311

RESULT 3

US-09-738-626-6710
; Sequence 6710, Application US/09738626

Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6710
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6710

Query Match 38.3%; Score 622.5; DB 10; Length 314;
Best Local Similarity 43.9%; Pred. No. 1.2e-55;
Matches 134; Conservative 54; Mismatches 108; Indels 9; Gaps 5;
Qy 18 KVVVGVGVSATAYTLLLSGIVSEIVLIDVKNKKAEGESMDLNHA---APSNTRSRAG 74
Db 8 KIVLIGAGDVGVAVALINQGMADHLAIIDIDKKLEGNVMDLNHGVVWADSRTRVTKG 67
Qy 75 DYPDCAGAAIVITCGINQKNGOTRMDLAANKNANIMLEIIPNVAKYAPDTILLIATNPVD 134
Db 68 TYADCEDAAMVVICAGAAQKPGETRLQVLVDKNNIKMSIVGDMDSGDFGIFLVASNPVD 127
Qy 135 VLTIVSYKASGFPPLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
Db 128 ILTYATWFKSGLPKRVISGTVLDSARFYMGLGELYEAPSSVHAYIIGEHGDTPLV 187
Qy 194 SLTNIDGKMLRDYCEKANHIFDQNAFHRIEFTQTRDAAYDIIRKGYTSYGIAGLLRIVK 253
Db 188 SSATIAGVSLRMLDKDPEL--EGRLEKIPEDTRDAAYHIIIDAKGSTSYGIGMGLARITR 245
Qy 254 AILEDGTLTSTVSTV--GDYFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIEMKESAS 311
Db 246 AILNQDQVAVPVVSALLHGEY-GEEDIYIGTPAVVNRGRIRRVVELEITDHEMERFRHSAN 304
Qy 312 QIKSV 316
Db 305 TLREI 309

RESULT 4

US-10-274-266-4
; Sequence 4, Application US/10274266
; Publication No. US20030059893A1
; GENERAL INFORMATION:
; APPLICANT: LADUNGA, Steven et al.
; TITLE OF INVENTION: Isolated Human Secreted Proteins, Nucleic Acid Molecules Encoding
; TITLE OF INVENTION: Secreted Proteins, And Uses Thereof
; FILE REFERENCE: CL000839DIV
; CURRENT APPLICATION NUMBER: US/10/274,266
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4


```
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/236,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 75
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 3365683CD1
US-09-974-298-75

Query Match      33.6%; Score 546; DB 10; Length 334;
Best Local Similarity 36.2%; Pred. No. 9.7e-48;
Matches 113; Conservative 72; Mismatches 117; Indels 10; Gaps 5;

Qy 18 KVVVGVGSGSATAYTLLSGIVSEIVLIDVNVKKAEGESMDLNHAA-----PSNTRSR 72
Db 23 KITVVGQGVGACAIISLGKSLADELALVDLEDKLGEMMDLQHGSLFLQTPKIVADK 82
Qy 73 AGDYPCAGAAIVVTGGINQKQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
Db 83 --DYSVTANSKIVVTVAGVROEGESRLNVQNVNFKFIIPQIVKYSDDCIIVVSNP 140
Qy 133 VDVLTYSYKASGPFSLRSVGTGVLDTARPKYILGHEHFKISSDSIDACVIGEHGD-GVP 191
Db 141 VDLITVTVTKLSGLPKHRVIGSGCNLDSARPRYLMAEKLGHPSSCHGWILGEGDSSVA 200
Qy 192 VWSLTNDGKRLDYCEKANHIFPONAFHRIFEQTRDAAYDIIRKKGVTSGVIAAGLLRI 251
Db 201 VMSGVNVAGVSLQELNPEIGTNDSENKWEVHKVMVSAVEYIKLGYTNWAGLSVADL 260
Qy 252 VKAILEDGTSTLTVST-VGDYFGVE-QIAISVPTKLNKGAHQVAELSDEKEIEMKS 309
Db 261 IESMLKNLSRIHPVSTVWVGMYGIENEVFLSLPCILNARGLTSTVINOQKLKDXDEVAQLKKS 320
Qy 310 ASQIKSVIEHLE 321
Db 321 ADTLWDIQDKLK 332

RESULT 8
US-10-177-293-262.
; Sequence 262, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Fuzstai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Ayesgul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
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; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-262

Query Match      33.6%; Score 546; DB 15; Length 334;
Best Local Similarity 36.2%; Pred. No. 9.7e-48;
Matches 113; Conservative 72; Mismatches 117; Indels 10; Gaps 5;

Qy 18 KVVVGVGSGSATAYTLLSGIVSEIVLIDVNVKKAEGESMDLNHAA-----PSNTRSR 72
Db 23 KITVVGQGVGACAIISLGKSLADELALVDLEDKLGEMMDLQHGSLFLQTPKIVADK 82
Qy 73 AGDYPCAGAAIVVTGGINQKQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
Db 83 --DYSVTANSKIVVTVAGVROEGESRLNVQNVNFKFIIPQIVKYSDDCIIVVSNP 140
Qy 133 VDVLTYSYKASGPFSLRSVGTGVLDTARPKYILGHEHFKISSDSIDACVIGEHGD-GVP 191
Db 141 VDLITVTVTKLSGLPKHRVIGSGCNLDSARPRYLMAEKLGHPSSCHGWILGEGDSSVA 200
Qy 192 VWSLTNDGKRLDYCEKANHIFPONAFHRIFEQTRDAAYDIIRKKGVTSGVIAAGLLRI 251
Db 201 VMSGVNVAGVSLQELNPEIGTNDSENKWEVHKVMVSAVEYIKLGYTNWAGLSVADL 260
Qy 252 VKAILEDGTSTLTVST-VGDYFGVE-QIAISVPTKLNKGAHQVAELSDEKEIEMKS 309
Db 261 IESMLKNLSRIHPVSTVWVGMYGIENEVFLSLPCILNARGLTSTVINOQKLKDXDEVAQLKKS 320
Qy 310 ASQIKSVIEHLE 321
Db 321 ADTLWDIQDKLK 332

RESULT 9
US-09-971-536-51
; Sequence 51, Application US/09971536
; Patent No. US20020159976A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Lubbers, Mark
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul
; APPLICANT: Reid, Julian
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Lactobacillus rhamnosus Polynucleotides, Polypeptides and Methods
; TITLE OF INVENTION: Using Them
; FILE REFERENCE: 1043c2
; CURRENT APPLICATION NUMBER: US/09/971,536
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/NZ01/00160
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US-10-144-649A-215

Query Match 17.3%; Score 280.5; DB 15; Length 148;
Best Local Similarity 41.4%; Pred. No. 6e-21;
Matches 53; Conservative 29; Mismatches 39; Indels 7; Gaps 2;
Qy 18 KVVVGVSGVSATAYTLLSGIVSEIVLIDVNDKKAEGESMDLNHAA-----PSNTRSR 72
Db 23 KITVGVGVQGVACAIISLGKSLADELALVDVLEKLGEMMDLQHGSLFLOTTPKIVADK 82
Qy 73 AGDYPDCAGAAIVVTCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
Db 83 --DYSVTANSKIVVTVAGVRQEGESRLNVQRNVNVFKFIIPQIVKSPDCIIVVSNP 140
Qy 133 VDVLTYIS 140
Db 141 VDILTYVT 148

RESULT 13

US-10-156-761-7888

; Sequence 7888, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7888
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7888

Query Match 13.8%; Score 223.5; DB 15; Length 303;
Best Local Similarity 27.9%; Pred. No. 1.3e-14;
Matches 75; Conservative 44; Mismatches 117; Indels 33; Gaps 9;
Qy 19 VVVVGVSGVSATAYTLLSGIVSEIVLIDVNDKKAEGESMDLNH-----NAPNTRSR-R 72
Db 4 VGVVGVAGVGTQVAAITLVASGICPELLVSVRTVEQARALAADLDMRQTTGSPVQPEARR 63
Qy 73 AGDYPDCAGAAIVVTCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
Db 64 VADLLGHCHAVVAVRAAATNTAADVRMGSGALTAPVIRALATILRGY--QGTVLVVTNP 121
Qy 133 VDVLTYISKASGFPPLSVISGTVLDTAPKYLGEHFKISSIDACVIGEHDGVPV 192
Db 122 VDLMTLRLFAETSGCF--RVYIGSNLDSARVRLTLAHLDDVPATTVHGVIGEHDGAVV 179
Qy 193 W-SLTNIDG---MKLRDYCEKANHIPONAFHRIFEQTRDAAYDIIKRGYTSYGTAG 247
Db 180 CASSTTVNGTAAVPLAE-----VRAELRTPQGISAGVGRTRSGPAGA 223
Qy 248 LLRIIV-KAI-LEDTGSTLTIVTVGDFGV 274
Db 224 VLSTLRKALGLVDGTEELTAHRGDWLCI 252

RESULT 14

US-10-106-698-6816

Query Match 11.5%; Score 186.5; DB 9; Length 142;
Best Local Similarity 39.2%; Pred. No. 2.7e-11;
Matches 40; Conservative 20; Mismatches 35; Indels 7; Gaps 2;

; Sequence 6816, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
; SEQ ID NO 6816
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (90)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (105)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6816

Query Match 12.5%; Score 202.5; DB 15; Length 146;
Best Local Similarity 38.9%; Pred. No. 6.3e-13;
Matches 42; Conservative 22; Mismatches 37; Indels 7; Gaps 2;
Qy 18 KVVVGVSGVSATAYTLLSGIVSEIVLIDVNDKKAEGESMDLNHAA-----PSNTRSR 72
Db 39 KITVGVGVQGVACAIISLGKSLADELALVDVLEKLGEMMDLHGSFLXTPKIVADK 98
Qy 73 AGDYPDCAGAAIVVTCGINOKNGQTRMDLAANKANIMLEIIPNVAKY 120
Db 99 --DYSVTANSKIVVTVAGVRQEGESRLNVQRNVNVFKFIIPQIVKY 144

RESULT 15

US-09-925-301-1533
; Sequence 1533, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1533

Qy 18 KVVVGVGVSATAYTLLSGIVSEIVLIDVNNKKAEGESMDLNHAA-----PSNTRSR 72
Db 43 KITVVGVGQVGMACAISILGKSLADELALVDVLEDKLGEMMDLQHGSLFLQTPKILADK 102
Qy 73 AGDYPDCAGAAIVIVTCGINQKNGQTRMDLAAKXANIMLEII 114
Db 103 --DYSVTANSKIVVVTAGVRQEGESRLNLVQRNVNVFKFII 142

Search completed: July 25, 2003, 11:55:02
Job time : 53 secs

L-lactate dehydrogenase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: E96932
R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E96932
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78248.1; PID:gl5023105; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0267
C:Superfamily: L-lactate dehydrogenase

Query Match 45.1%; Score 733; DB 2; Length 313;
Best Local Similarity 47.0%; Pred. No. 3.1e-48;
Matches 147; Conservative 65; Mismatches 91; Indels 10; Gaps 5;
Qy 15 KTVKVVGVGSGSATYTLTLLSGIVSEIVLIDVNDKDKAGEGMDLNHAA---PSNTR 70
Db 3 KNTKISVIGAGFVSSITVFMNGGLASEIVIVDVKDKAGEAMDLSHGNAFVKPVVVK 62
Qy 71 SRAGDYPDCAGAAIVIVTCGINQKNQOTRMDLAANKANIMLEIIPNVAKYAPDTILLIAT 130
Db 63 S--GDYKDTGSDIVITITAGAAQKPGETRLBELINKNYNIFKSIIVPEVVKYNPNAILLVVS 120
Qy 131 NPVDVLTIVISKAGFPPLSRVIGSGTDLTARFKYLGEHFKISSDSIDACVIGEHGDG- 189
Db 121 NPVDILTIVITKLSGFPKSRVIGSGTDLTDRFRYMLSEHFEIDVNRNIHTYIMGEHGDSE 180
Qy 190 VPMVSLTNIDGKRLDYCEKANHFIDQNAFRIPEQTRDAAYDIIKRGYTSYGIAAGLL 249
Db 181 IATWSLTNIAGMDVNEYCEASCKCDGSLKYIYDDVKNAAHYVIERKGGATYVAVALVK 240
Qy 250 RIVKAILDSTGLTVSTV--GDYFGVQIAISVPTKLNKGAHQVAELSDKEIEME 307
Db 241 RIVKAILDENSILTVSSLLGQY--GIKDVYMGVPSVINGVVDIIIEVPLNDEKKNLT 299
Qy 308 KSASQIKSVIEHL 320
Db 300 DSAKTLKESLDSI 312

RESULT 3
DBESLM
L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus megaterium
C:Species: Bacillus megaterium
C>Date: 03-Aug-1984 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C:Accession: S00133; S01472; A00354
R:Waldvogel, S.; Weber, H.; Zuber, H.
Biol. Chem. Hoppe-Seyler 368, 1391-1399, 1987
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic megaterium. Preparation and properties of a hybrid lactate dehydrogenase comprising mol
A:Reference number: S00133; MUID:88107005; PMID:3122782
A:Accession: S00133
A:Molecule type: DNA
A:Residues: 1-318 <WAL>
A:Cross-references: EMBL:M22305; NID:gl43135; PIDN:AAA22566.1; PID:gl43136
R:Stangl, D.; Wiederkehr, F.; Suter, F.; Zuber, H.
Biol. Chem. Hoppe-Seyler 368, 1157-1166, 1987
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic megaterium.
A:Reference number: S01472; MUID:88050100; PMID:3118900
A:Accession: S01472
A:Molecule type: protein
A:Residues: 1-318 <STA>
C:Comment: This enzyme is activated by fructose-1,6-diphosphate.
C:Function:

A:Description: catalyzes the reversible oxidation of (S)-lactate to pyruvate by NAD+
C:Superfamily: L-lactate dehydrogenase
C:Keywords: homotetramer; NAD; oxidoreductase
F;1-318/Product: L-lactate dehydrogenase #status experimental <MAT>
F;11-41/Region: beta-alpha-beta NAD nucleotide-binding fold
F;154,181/Active site: Asp. His #status predicted

Query Match 44.5%; Score 723.5; DB 1; Length 318;
Best Local Similarity 49.2%; Pred. No. 1.7e-47;
Matches 150; Conservative 54; Mismatches 94; Indels 7; Gaps 5;
Qy 15 KTVKVVGVGSGSATYTLTLLSGIVSEIVLIDVNDKDKAGEGMDLNHAAPESTSR-- 72
Db 8 KTRKVAIVIGTGFVSSYAFSMVNQGIANELVLIDMKNKAGEARDINHGMPFATPKMIW 67
Qy 73 AGDYPDCAGAAIVIVTCGINQKNQOTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
Db 68 AGDYKDCADADLAVITAGANQAPGETRLDLVEKNVIFECIVKIDMNSGFDGILVATNP 127
Qy 133 VDVLTVISYKAGFPPLSRVIGSGTDLTARFKYLGEHFKISSDSIDACVIGEHGDG-VGP 191
Db 128 VDLAHVTQKVSGLPNRIGSGTDLTARFRYLLSDYFVDSRNHYAIMGEHGDTEFP 187
Qy 192 VMSLTNIDGKRLDYCEKANHFIDQNAFRIPEQTRDAAYDIIKRGYTSYGIAAGLLRI 251
Db 188 VMSHAQIGGVKLEHFINTA-AIEKEPDMQHLFQTRDAAYHIIINRKGATYVGIAAGLVRI 246
Qy 252 VKAILDSTGLTVSTV--GDYFGVQIAISVPTKLNKGAHQVAELSDKEIEMEKS 309
Db 247 TKAILDENSILTVSSLLGQY--GISDVYIGVPAIINKGVQRIIELNLTTPHEQQOULEHS 305
Qy 310 ASQIK 314
Db 306 ASILK 310

RESULT 4
S36863
L-lactate dehydrogenase (EC 1.1.1.27) - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 22-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
C:Accession: S36863; S36864; D72202
R:Ostendorp, R.; Liebl, W.; Schurig, H.; Jaenicke, R.
Eur. J. Biochem. 216, 709-715, 1993
A:Title: The L-lactate dehydrogenase gene of the hyperthermophilic bacterium Thermotoga
A:Reference number: S36863; MUID:94009031; PMID:8404889
A:Accession: S36863
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <OST>
A:Cross-references: EMBL:X74302; NID:g396280; PIDN:CAA52355.1; PID:g396281
A:Accession: S36864
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-31,38-53,55-85,163-173 <OS2>
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.W.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: D72202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <ARN>
A:Cross-references: GB:AE001823; GB:AE000512; NID:g4982441; PIDN:AAD36929.1; PID:g498245;
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1867
C:Superfamily: L-lactate dehydrogenase
C:Keywords: oxidoreductase
Query Match 42.3%; Score 687.5; DB 2; Length 319;

R;Barstow, D.A.; Murphy, J.P.; Sharman, A.F.; Clarke, A.R.; Holbrook, J.J.; Atkinson, T.
Eur. J. Biochem. 165, 581-586, 1987
A;Title: Amino acid sequence of the L-lactate dehydrogenase of *Bacillus caldotenax* deduced from cDNA
A;Reference number: S00019; MUID:87246643; PMID:3297694
A;Accession: S00019
A;Molecule type: DNA
A;Residues: 1-317 <BAR>
A;Cross-references: EMBL:M28336; NID:gl43129; PIDN:AAA22563.1; PID:gl43130
R;Zuelli, F.; Weber, H.; Zuber, H.
Biol. Chem. Hoppe-Seyler 368, 1167-1177, 1987
A;Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic
stearothermophilus, *Bacillus caldolyticus* and *Bacillus caldotenax*.
A;Reference number: A29704; MUID:88050101; PMID:3675869
A;Accession: C29704
A;Molecule type: DNA
A;Residues: 1-50, 'L', 52-137, 'S', 139-317 <ZUE>
A;Cross-references: GB:M19395; NID:gl43133; PIDN:AAA22565.1; PID:gl43134
A;Experimental source: strain DSM 406
C;Genetics:
A;Gene: lcta
C;Function:
A;Description: catalyzes the reversible oxidation of lactate to pyruvate by NAD+
C;Superfamily: L-lactate dehydrogenase
C;Keywords: homotetramer; NAD; oxidoreductase

Query Match 41.2%; Score 669; DB 2; Length 317;
Best Local Similarity 45.6%; Pred. No. 2.3e-43;
Matches 139; Conservative 54; Mismatches 106; Indels 6; Gaps 4;

QY 18 KVVVGVGSGSATAYTLLLSGIVSEIVLIDVNDKKAEGESMDLNHA---APSNTSRAG 74
DB 8 RVAVVGTGFGVASYAFALMNOGIADSVLIDANENKAGDAMDNFHKGVPAPKADLWHG 67
QY 75 DYPCAGAAIVIVTCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 68 DYDCDRDADLVVICAGANQKPGETRLDVKNAIAFRSIVSVASFGQGLFVATNPVD 127
QY 135 VLTYSYKASGFPRLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
DB 128 ILTYATWKSGLPHERVIGSGTILDTARFLLGDFYFVAVPNVHAYIIEGHGDTPLPW 187
QY 194 SLTNIDGMKLRDYCEKANHI FQDNAFHRIFEQTRDAAYDIIRKGYTSYGIAAGLRIVK 253
DB 198 SQADIGGVPKRLVESKGE-EAQKELERIFVNVDRDAAYQIEKKGATYGIAMGLARVTR 246
QY 254 AILEDGTGSLTVSTVGD-YFGVEQIAISVPTKLNKSGAHQVAELSDEKEIEMKESASQ 312
DB 247 AILHNNAILTVSAYLDGPGYGERDVIYGVPAVINNRNGIREVIEIELDEEEKKWFHRSAA 306
QY 313 IKSVI 317
DB 307 LKGVL 311

RESULT 8
T44580
lactate dehydrogenase [imported] - *Bacillus stearothermophilus*
C;Species: *Bacillus stearothermophilus*
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T44580
R;Nishida, Y.
submitted to the EMBL Data Library, October 1999
A;Description: Nucleotide sequence of the lactate dehydrogenase gene from *Bacillus stear*
A;Reference number: Z22797
A;Accession: T44580
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-317 <NIS>
A;Cross-references: EMBL:AB033627; PIDN:BAA85589.1
C;Genetics:
A;Note: ldh
C;Superfamily: L-lactate dehydrogenase

Query Match 41.1%; Score 667.5; DB 2; Length 317;
Best Local Similarity 45.4%; Pred. No. 3e-43;
Matches 142; Conservative 56; Mismatches 108; Indels 7; Gaps 5;
QY 10 VRTDAKTQVVVGVGSGSATAYTLLLSGIVSEIVLIDVNDKKAEGESMDLNHA---AP 66
DB 1 MKNDGGT-RVVVIGTGFVASYAFALMNOGITDSEIVLIDANESKAIGDAMDNLHGVFAP 59
QY 67 SNTRSRAGDYPDCAGAAIVIVTCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTIL 126
DB 60 KPAVVRHGDYSDCHADLVVICAGANQKPGETRLDVKNAIAFRSIVSVASFGQGLF 119
QY 127 LIATNPVDVLTYSYKASGFPRLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEH 186
DB 120 LVATNPVDILTATWKSGLPHERVIGSGTILDTARFLLGDFYFVAVPNVHAYIIEGH 179
QY 187 GD-GVPVWSLTNIDGMKLRDYCEKANHI FQDNAFHRIFEQTRDAAYDIIRKGYTSYGIA 245
DB 180 GDTPLPWSQADIGGVPKRLVE-AKGEQAKELERIFTDVRDAAYQIEKKGATYGIAM 238
QY 246 AGLLRIVKAILEDGTGSLTVSTVGD-YFGVEQIAISVPTKLNKSGAHQVAELSDEKEIE 304
DB 239 MGLARVTRAILHNNAILTVSAYLDGPGYGERDVIYGVPAVINNRNGIREVIEIELNDEKN 298
QY 305 LMEKSASQIKSVI 317
DB 299 RFHHSAAITLKSVL 311

RESULT 9
B29704

L-lactate dehydrogenase (EC 1.1.1.27) - *Bacillus caldolyticus*

C;Species: *Bacillus caldolyticus*

C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 28-May-1999

C;Accession: B29704

R;Zuelli, F.; Weber, H.; Zuber, H.

Biol. Chem. Hoppe-Seyler 368, 1167-1177, 1987

A;Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic
stearothermophilus, *Bacillus caldolyticus* and *Bacillus caldotenax*.
A;Reference number: A29704; MUID:88050101; PMID:3675869

A;Accession: B29704

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-317 <ZUE>

A;Cross-references: GB:M19394; GB:M19386; NID:gl43131; PIDN:AAA22564.1; PID:gl43132

C;Superfamily: L-lactate dehydrogenase

C;Keywords: NAD; oxidoreductase

Query Match 40.6%; Score 659; DB 2; Length 317;
Best Local Similarity 45.2%; Pred. No. 1.3e-42;
Matches 138; Conservative 53; Mismatches 108; Indels 6; Gaps 4;

QY 18 KVVVGVGSGSATAYTLLLSGIVSEIVLIDVNDKKAEGESMDLNHA---APSNTSRAG 74
DB 8 RVVIVGTGFGVASYAFALMNOGIADSVLIDANESKAIGDAMDNFHKGVPAPKADLWHG 67
QY 75 DYPCAGAAIVIVTCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 68 DYDCDRDADLVVICAGANQKPGETRLDVKNAIAFRSIVSVASFGQGLFVATNPVD 127
QY 135 VLTYSYKASGFPRLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
DB 128 ILTYATWKSGLPHERVIGSGTILDTARFLLGDFYFVAVPNVHAYIIEGHGDTPLPW 187
QY 194 SLTNIDGMKLRDYCEKANHI FQDNAFHRIFEQTRDAAYDIIRKGYTSYGIAAGLRIVK 253
DB 188 SQADIGGVPKRLVESKGE-EAQKELERIFVNVDRDAAYQIEKKGATYGIAMGLARVTR 246
QY 254 AILEDGTGSLTVSTVGD-YFGVEQIAISVPTKLNKSGAHQVAELSDEKEIEMKESASQ 312
DB 247 AILHNNAILTVSAYLDGPGYGERDVIYGVPAVINNRNGIREVIEIELNDEKNRHHSAAT 306
QY 313 IKSVI 317

Db 307 LKSVL 311
:||||:

RESULT 10

A84142
L-lactate dehydrogenase lctE [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: A84142
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000.
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A84142
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <STO>
A:Cross-references: GB:AP001520; GB:BA000004; NID:gl0176401; PIDN:BA07656.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Gene: lctE
C:Superfamily: L-lactate dehydrogenase

Query Match 39.9%; Score 649; DB 2; Length 310;
Best Local Similarity 45.2%; Pred. No. 7.4e-42;
Matches 138; Conservative 53; Mismatches 100; Indels 14; Gaps 6;

Qy	18	KVVVGVGSGSATAYTLTLLSGIVSEIVLIDVNVKDKAEGESMDLNHA---APNSTRAG 74
Db	8	KIVLVGTGAGSSYAYALMNGQISDELILVDLNEEKAKGVLDLHNSIVVAPSPMEIKFG 67
Qy	75	DYPDCAGAAIVIVTCGINQKNGQTRMDLAAKNANIMLEIIPNVAKYAPDPTILLIATNPVD 134
Db	68	SYEDCKDALVVICAGAAQKPEGRDLVHKVQCFIPESIVGNIMKSGFGLFVATNPVD 127
Qy	135	VLTVISYKAGFPILSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGDG-VPVW 193
Db	128	ILAVATWFKSGLPKRIVIGSGTVLDTARFRYLLIGEENMAAPTSHVGYIIEGHGDSQLPVW 187
Qy	194	SLTNIDGMKLRDYCEKANHFQDNAPHRIFEQTRDAAYDIIRKGYTSYGIAGLRIVK 253
Db	188	SSATIAGTPI-----APRUTDEKK-OEIAENVRDAAYKIIERKAGATYGIATGLAKRITR 240
Qy	254	AILEDTGSTLTIVSTV--GDYFGVEQIAISVPTKLKNSGAHQVAELSDKEIEIEMKESAS 311
Db	241	ALLKNENVLPVGTLLSGEN-GHDDVYIGVPAIINREGVRQVVELSLNDEKEKFAFSVE 299
Qy	312	QIKSV 316
Db	300	TLKDI 304

RESULT 11

DEBSLF
L-lactate dehydrogenase (EC 1.1.1.27) [validated] - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C>Date: 03-Aug-1994 #sequence_revision 07-Feb-1997 #text_change 03-Nov-2000
C:Accession: A26053; A29704; A91726; A00353
R:Barstow, D.A.; Clarke, A.R.; Chia, W.N.; Wigley, D.; Sharman, A.F.; Holbrook, J.J.; Ab
Gene 46, 47-55, 1986
A>Title: Cloning, expression and complete nucleotide sequence of the Bacillus stearother
A:Reference number: A26053; MUID:87106842; PMID:3026926
A:Accession: A26053
A:Molecule type: DNA
A:Residues: 1-317 <BAR>
A:Cross-references: GB:M14788; NID:gl143139; PIDN:AAA22568.1; PID:gl143140
R:Zuelli, F.; Weber, H.
Biol. Chem. Hoppe-Seyler 368, 1167-1177, 1987
A>Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesoph
stearothermophilus, Bacillus caldolyticus and Bacillus caldofenax.
A:Reference number: A29704; MUID:88050101; PMID:3675869
A:Accession: A29704

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <ZUE>
A:Cross-references: GB:M19396; GB:M19386; NID:gl143137; PIDN:AAA22567.1; PID:gl143138
R:Wirz, B.; Suter, F.; Zuber, H.
Hoppe-Seyler's Z. Physiol. Chem. 364, 893-909, 1983
A>Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesoph
A:Reference number: A91726; MUID:84006440; PMID:6352452
A:Accession: A91726
A:Molecule type: protein
A:Residues: 1-107, SE', 110-112, 'H', 114-317 <WIR>
A:Experimental source: NCIB 8924
R:Fratschin, J.D.; Wirz, B.; Frank, G.; Zuber, H.
Hoppe-Seyler's Z. Physiol. Chem. 364, 879-892, 1983
A>Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesoph
A:Reference number: A91725; MUID:84006439; PMID:6618448
A:Contents: annotation; CNR fragments; partial sequence
A>Note: strain NCIB 8924
C:Function:

A:Description: catalyzes the reversible oxidation of (S)-lactate to pyruvate by NAD+
C:Superfamily: L-lactate dehydrogenase
C:Keywords: NAD; oxidoreductase; tetramer
F:8-38/Region: beta-alpha-beta NAD nucleotide-binding fold
F:152,179/Active site: Asp, His #status predicted

Query Match 39.9%; Score 648; DB 1; Length 317;
Best Local Similarity 44.9%; Pred. No. 9.1e-42;
Matches 137; Conservative 51; Mismatches 111; Indels 6; Gaps 4;

Qy	18	KVVVGVGSGSATAYTLTLLSGIVSEIVLIDVNVKDKAEGESMDLNHA---APNSTRAG 74
Db	8	RVVVIGAGFVGASYVEPALMNGQIADBEIVLIDANESKAIGDAMDENHGKVPAPVDIWHG 67
Qy	75	DYPDCAGAAIVIVTCGINQKNGQTRMDLAAKNANIMLEIIPNVAKYAPDPTILLIATNPVD 134
Db	68	DYDCCDADLWVICAGANQKPGETRLDLVDKNIAIFRSIVESYMASGFGQLFLVATNPVD 127
Qy	135	VLTVISYKAGFPILSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGDG-VPVW 193
Db	128	ILTYATWFKSGLPKRIVIGSGTILDTARFRFLGVEFVSAPQNVHAYIIEGHGDTPLPVW 187
Qy	194	SLTNIDGMKLRDYCEKANHFQDNAPHRIFEQTRDAAYDIIRKGYTSYGIAGLRIVK 253
Db	188	SQAYIGVMPKRLVESKGE-EAQKDLERIFVNVVDAAYQIEKKGATYGIAGLARVTR 246
Qy	254	AILEDTGSTLTIVSTVGD-YFGVEQIAISVPTKLKNSGAHQVAELSDKEIEIEMKESASQ 312
Db	247	AILHNNAILTVSAYLDGLYGERDVYIGVPAVINNRNGIREVIEILNDDKKNRPFHSAAT 306
Qy	313	IKSVI 317
Db	307	LKSVL 311

RESULT 12

D89787
L-lactate dehydrogenase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89787
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89787
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700156; PIDN:BAB41455.1; GSPDB:GN00149
A:Experimental source: strain N315

‘

Query Match 39.3%, Score 639; DB 2; Length 321;
Best Local Similarity 44.1%; Pred. No. 4.5e-41;
Matches 135; Conservative 56; Mismatches 109; Indels 6; Gaps 4;

Qy	18	KVVVGVGSGSATAYTLISGIVSEIVLIDVKNKKAEGESMDLNHAAP---SNTSRAG 74
Db	8	KVALIGAGFVGSSYAFALINQGITDELIVIDVKNKKAEGESMDLNHAAPGLOQPVKTSYG 67
Qy	75	DYPCAGAAIVIVTCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDPTILLIATNPVD 134
Db	68	TYEDCKDADIVCICAGANQKPGETRELVEKNLKFPGIVSEVMASGDFGIFLVATNPVD 127
Qy	135	VLTVISKAGFPLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
Db	128	ILTYATWKFGLPKRERVIGSGTTLDSARFRFMLSEYFGAAPQNVHAHIIGEHGDTELPVW 187
Qy	194	SLTNIDGMKLRDYCEKANHIFDQNAFHRIFEQTFDAAYDIIKRGYTSYGIAGLLRIVK 253
Db	188	SHANVGVPVSELVEK-NDAYKQELDOI VDDVKNAAHYHIERKGATYYGVAMSLARITK 246
Qy	254	AILEDGTGTLTVSTVGD-YFQVEQIAISVPTKLNKGAHQAELSLDEKEIEMKXSASQ 312
Db	247	AILHNENSILTVSTYLDQYGADDVYIGVPAVNVNRGGIAGITELNLNEKEQFLHSAGV 306
Qy	313	IKSVIE 318
Db	307	LKNILK 312

RESULT 15

H86671
L-lactate dehydrogenase (EC 1.1.1.27) [imported] - Lactococcus lactis subsp. lactis (str
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: H86671
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86671
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: GB:AB005176; FID:g12723247; PIDN:AAK04474.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ldhB
C;Superfamily: L-lactate dehydrogenase
C;Keywords: oxidoreductase

Query Match 38.6%, Score 627; DB 2; Length 314;
Best Local Similarity 43.9%; Pred. No. 3.5e-40;
Matches 136; Conservative 59; Mismatches 107; Indels 8; Gaps 5;

Qy	18	KVVVGVGSGSATAYTLISGIVSEIVLIDVKNKKAEGESMDLNHA---APSNTRSRAG 74
Db	7	KVVVIGTGFVGTSTAYSMINQGLVNLVLIDVNDQKAEGEALDLDGVSNGQENVIVRAG 66
Qy	75	DYPCAGAAIVIVTCGINQKNGQTRMDLAANKNANIMLEIIPNVAKYAPDPTILLIATNPVD 134
Db	67	DYKCKNADIVVVVTVAGVQKQSRDLVNTNAKIMRSIVTVQVMDSGDFGIFVIASNPVD 126
Qy	135	VLTVISKAGFPLSRVIGSGTVLDTARFKYILGEHFKISSDSIDACVIGEHGDG-GVPVW 193
Db	127	ILTVAVNETGLDOSRIVGTGTLDTTRFRKELATKLEIDPRSVHGVIIGEHGDSEVAVW 186
Qy	194	SLTNIDGMKLRDYCEKANHIFDQNAFHRIFEQTFDAAYDIIKRGYTSYGIAGLLRIVK 253
Db	187	SHTTVGCKPILFEIVKKNKIGVED-LSNLSNKVNAAVEIIDKKQATYYIGHMSTARIVK 245
Qy	254	AILEDGTGTLTVSTV--GDYFGEQIAISVPTKLNKGAHQAELSLDEKEIEMKXSAS 311
Db	246	AILNNEOAILFVSAYLREGY-GQEGVFTGVPSIVNONGVREIIEILNIDAYEKKQFEKSVS 304

Qy	312	QIKSVIEHLE 321
Db	305	QLKEVIESIK 314

Search completed: July 25, 2003, 11:46:44
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2003, 11:38:26 ; Search time 23. Seconds
(without alignments)
660.419 Million cell updates/sec

Title: US-09-992-430B-22

Perfect score: 1625

Sequence: 1 MFQDTKSQAVRTDAKTVKV.....ELMEKASQIKSVIEHLEIN 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	838	51.6	330	1	LDH_SCHPO
2	733	45.1	313	1	LDH_CLOAB
3	723.5	44.5	318	1	LDH_BACME
4	722	44.4	317	1	LDH_CLOPE
5	687.5	42.3	319	1	LDH_THEMA
6	679	41.8	318	1	LDH_BACPS
7	673	41.4	319	1	LDH_BACPS
8	667	41.0	317	1	LDH_BACCA
9	659	40.6	317	1	LDH_BACCL
10	649	39.9	310	1	LDH_BACD
11	648	39.9	317	1	LDH_BACST
12	647.5	39.8	317	1	LDH1_STAAM
13	639.5	39.4	325	1	LDH1_LACCA
14	639	39.3	320	1	LDH1_BACSU
15	627	38.6	314	1	LDH2_LACLA
16	622.5	38.3	314	1	LDH_CORGL
17	618.5	38.1	325	1	LDH1_LACSK
18	617	38.0	313	1	LDH1_LISIN
19	617	38.0	313	1	LDH1_LISNO
20	613	37.7	310	1	LDH1_THEAQ
21	606	37.3	316	1	LDH1_BOREU
22	604	37.2	310	1	LDH1_THECA
23	598	36.8	319	1	LDH2_STAAM
24	596	36.7	319	1	LDH2_STAAM
25	596	36.7	326	1	LDH1_STRPY
26	595	36.6	323	1	LDH1_STRPY
27	594	36.6	332	1	LDH1_LACCH
28	591.5	36.4	324	1	LDH1_LACIL
29	589.5	36.3	324	1	LDH1_LACLA
30	586.5	36.1	330	1	LDH1_DISEL
31	586.5	36.1	330	1	LDH1_PACRC
32	585.5	36.0	330	1	LDH1_DISMA
33	583	35.9	332	1	LDH1_SQUAC

RESULT 1
LDH_SCHPO
ID LDH_SCHPO STANDARD; PRT; 330 AA.
AC Q9P7P7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN SPAC186.08C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voickaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehtach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Cruzado M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Rochazo L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).

CC -1- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.

CC -1- PATHWAY: Anaerobic glycolysis; final step.

CC -1- SUBUNIT: Homotetramer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.

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093619 chaenoceph
093541 champsoceph
093545 lepidonotot
09pr8 notochenia
093546 patagonotot
093540 gobionotot
093539 notochenia
09w7m6 ambystoma m
093542 eleginotpe m
093543 paranotthe
093401 coryphopter
P06151 mus musculu

34 582.5 35.8 330 1 LDHA CHAAC
35 582.5 35.8 330 1 LDHA CHAGU
36 582.5 35.8 330 1 LDHA LEPNU
37 581.5 35.8 330 1 LDHA NOTAN
38 581.5 35.8 330 1 LDHA_PATTE
39 581.5 35.8 330 1 LDHA_GOGGI
40 580.5 35.7 330 1 LDHA AMTCO
41 580 35.7 333 1 LDHA AMBME
42 579 35.6 331 1 LDHA_ELEMC
43 578.5 35.6 330 1 LDHA_PARMG
44 578.5 35.6 331 1 LDHA_CORNI
45 578 35.6 331 1 LDHA_MOUSE

ALIGNMENTS

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-----
CC EMBL; AL157811; CAB75872.1; -.
CC PIR; T50135; T50135.
CC HSSP; P00344; 2LDH.
CC GeneDB Spombe; SPAC186.08c; -.
CC InterPro; IPR001557; L_LDH.
CC InterPro; IPR001236; ldh.
CC InterPro; IPR000205; NAD_binding.
CC InterPro; IPR000594; Thif_domain.
CC Pfam; PF00056; ldh.1.
CC Pfam; PF02866; ldh.C.1.
CC PRINTS; PR00086; LLDHGRNASE.
CC PROSITE; PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis.
FT ACT_SITE 192 192 ACCEPTS A PROTON DURING CATALYSIS
FT ACT_SITE 192 192 (BY SIMILARITY).
SQ SEQUENCE 330 AA; 35591 MW; 5F68D53F3EA7CD0 CRC64;

Query Match 51.6%; Score 838; DB 1; Length 330;
Best Local Similarity 50.5%; Pred. No. 1.2e-54;
Matches 162; Conservative 64; Mismatches 91; Indels 4; Gaps 3;

7 SOAVRTDA-KTVKVVGVGVSGATATVLLSGIVSEIVLDVVKKAEGESMDLNHAA 65
10 NDSVRSSEFKIKIVIGVAGNVGTTATFTLLSGLAAEIVLDLKKKAEGEANDLNHAA 69
66 P--SNTRSAGDPPDCAAAIVVTCGINQKNGOTRMDLAANKANIMLEIIPNVAKYAPD 123
70 PLSHETRYLGDYKCDKDATAVITAGKNQKPGETRMDDLKANISIFKEILREVTKYTKD 129
124 TILLIATNPVLTIVISKAGPPLSRVIGSGTVDLTARFKYILGEHFKISSDSIDACVI 183
130 ALLVATNPVLTIVATLTKTGFAERVIGSGTIDTARFYLKGLYGLDPQSVNADII 189
184 GEHGDG-VPVMSLTNIDGMKLDYCEKANHI FQONAFHRIFEQTRDAAYDIIKRGVTSY 242
190 GEHGDSELAWSHASIAGLSLADCESEETKYDQALNCEPKETKNAAYDIIQRKGSTY 249
243 GIAGLLRIVKAILDGTSTTVSTVGYFVGEQIAISVPTKLNKSGAHQVAELSDEKE 302
250 GVAAGLVRIILAAIRDENALLTVSGDSYSGNIGDVCFSMPRLKNGOAHRIINAKLSKDE 309
303 IELMEKSASQTSKSVIEHLIN 323
310 DAKLVESVSKHAIETISGLN 330

RESULT 2
LDH_CLOAB STANDARD; PRT; 313 AA.
AC Q97MD1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH OR CAC0267.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
*CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.

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-----
CC -!- PATHWAY: Anaerobic glycolysis; final step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
-----
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CC or send an email to license@sib-sib.ch).
-----
CC EMBL; AE007540; AAK78248.1; -.
CC PIR; E96932; E96932.
CC HAMAP; MF 00488; -; 1.
CC InterPro; IPR001557; L_LDH.
CC InterPro; IPR001236; ldh.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF00056; ldh.1.
CC Pfam; PF02866; ldh.C.1.
CC PRINTS; PR00086; LLDHGRNASE.
CC PROSITE; PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis; Complete proteome.
FT ACT_SITE 176 176 BY SIMILARITY.
SQ SEQUENCE 313 AA; 34181 MW; C98FD402E62F45D2 CRC64;

Query Match 45.1%; Score 733; DB 1; Length 313;
Best Local Similarity 47.0%; Pred. No. 6.2e-47;
Matches 147; Conservative 65; Mismatches 91; Indels 10; Gaps 5;

15 KTVKVVGVGVSGATATVLLSGIVSEIVLDVVKKAEGESMDLNHAA----PSNTR 70
3 KNTKISVIGAGFGVSGSTVFALMNGGLASEIVVVDVVKKAEGEAMDLHSGAAFVKPVPVK 62
71 SRAGDPPDCAAAIVVTCGINQKNGOTRMDLAANKANIMLEIIPNVAKYAPDTILLIAT 130
63 S--GDYKDTGSDIIVITAGAAQKPGETRLINKNKNVIFKSVPEVVKYNPNAILLVVS 120
131 NPVDVLTIVISKAGPPLSRVIGSGTVDLTARFKYILGEHFKISSDSIDACVIGHDG- 189
121 NPVDILTIVITKLSGFPKSRVIGSGTVDLTSTRFYMLSEHFEIDVRNIHTYIMGEHGDSE 180
190 VPVMSLTNIDGMKLDYCEKANHI FQONAFHRIFEQTRDAAYDIIKRGVTSYIGIAAGLL 249
181 IATWSLTNIAGMDVNEICEASCKCGSLKYIKYIDVKNAAHYVIEKKGATYTAVALVK 240
250 RIVKAILDGTSTITVSTV--GDYFVGEQIAISVPTKLNKSGAHQVAELSDEKEIELME 307
241 RIVEAILRDENSILTVSSILEGOY-GIKDVMGVPSIVGVINGVKDIIIEVPLNDEEKNLT 299
308 KSASQTSKSVIEHL 320
300 DSAKTLKESLDSI 312

RESULT 3
LDH_BACME STANDARD; PRT; 318 AA.
ID LDH_BACME
AC P00345;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 090;
RX MEDLINE=88107005; PubMed=3122782;
RA Waldvogel S., Weber H., Zuber H.;

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-----
CC EMBL; AL157811; CAB75872.1; -.
CC PIR; T50135; T50135.
CC HSSP; P00344; 2LDH.
CC GeneDB Spombe; SPAC186.08c; -.
CC InterPro; IPR001557; L_LDH.
CC InterPro; IPR001236; ldh.
CC InterPro; IPR000205; NAD_binding.
CC InterPro; IPR000594; Thif_domain.
CC Pfam; PF00056; ldh.1.
CC Pfam; PF02866; ldh.C.1.
CC PRINTS; PR00086; LLDHGRNASE.
CC PROSITE; PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis.
FT ACT_SITE 192 192 ACCEPTS A PROTON DURING CATALYSIS
FT ACT_SITE 192 192 (BY SIMILARITY).
SQ SEQUENCE 330 AA; 35591 MW; 5F68D53F3EA7CD0 CRC64;

Query Match 51.6%; Score 838; DB 1; Length 330;
Best Local Similarity 50.5%; Pred. No. 1.2e-54;
Matches 162; Conservative 64; Mismatches 91; Indels 4; Gaps 3;

7 SOAVRTDA-KTVKVVGVGVSGATATVLLSGIVSEIVLDVVKKAEGESMDLNHAA 65
10 NDSVRSSEFKIKIVIGVAGNVGTTATFTLLSGLAAEIVLDLKKKAEGEANDLNHAA 69
66 P--SNTRSAGDPPDCAAAIVVTCGINQKNGOTRMDLAANKANIMLEIIPNVAKYAPD 123
70 PLSHETRYLGDYKCDKDATAVITAGKNQKPGETRMDDLKANISIFKEILREVTKYTKD 129
124 TILLIATNPVLTIVISKAGPPLSRVIGSGTVDLTARFKYILGEHFKISSDSIDACVI 183
130 ALLVATNPVLTIVATLTKTGFAERVIGSGTIDTARFYLKGLYGLDPQSVNADII 189
184 GEHGDG-VPVMSLTNIDGMKLDYCEKANHI FQONAFHRIFEQTRDAAYDIIKRGVTSY 242
190 GEHGDSELAWSHASIAGLSLADCESEETKYDQALNCEPKETKNAAYDIIQRKGSTY 249
243 GIAGLLRIVKAILDGTSTTVSTVGYFVGEQIAISVPTKLNKSGAHQVAELSDEKE 302
250 GVAAGLVRIILAAIRDENALLTVSGDSYSGNIGDVCFSMPRLKNGOAHRIINAKLSKDE 309
303 IELMEKSASQTSKSVIEHLIN 323
310 DAKLVESVSKHAIETISGLN 330

RESULT 2
LDH_CLOAB STANDARD; PRT; 313 AA.
AC Q97MD1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH OR CAC0267.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
*CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.

```

"Structure and function of L-lactate dehydrogenases from thermophilic and mesophilic bacteria. VII. Nucleotide sequence of the lactate dehydrogenase gene from the mesophilic bacterium *Bacillus megaterium*. Preparation and properties of a hybrid lactate dehydrogenase comprising moieties of the *B. megaterium* and *B. stearothermophilus* enzymes." *Biol. Chem. Hoppe-Seyler* 368:1391-1399(1987).

```

RN LDH_CLOPE
RN ID - LDH_CLOPE STANDARD; PRT; 317 AA.
AC Q8XP62;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH OR CPE0103.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
CC -1- PATHWAY: Anaerobic glycolysis; final step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M22305; AAA22566.1; -.
DR PIR; S00133; DEBSLM.
DR HSP; P00344; LDH.
DR HAMAP; MF_00488; -.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR00205; NAD_binding.
DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh_C; 1.
DR PRINTS; PR00086; LDHHRGNASE.
DR PROSITE; PS00064; L_LDH; 1.
DR Oxidoreductase; NAD; Glycolysis.
KW ACT SITE 181
FT ACT SITE 181 BY SIMILARITY.
SQ SEQUENCE 318 AA; 35035 MW; 1712190576E1485 CRC64;

Query Match 44.5%; Score 723.5; DB 1; Length 318;
Best Local Similarity 49.2%; Pred. No. 3.1e-46;
Matches 150; Conservative 54; Mismatches 94; Indels 7; Gaps 5;

QY 15 KTKVVVVGVSGSATATYLLSGIVSEIVLDVNVKDKAEGESMDLNHAAP--SNTSR-- 72
DB 8 KTRKVAIVGTFGVSSVAFSVNMGVIGANVELVLDVNVKDKAEGARDINHGPFATPKIW 67
QY 73 AGDYPDCAGAAIVITVTCGINKQKQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
DB 68 AGDYKCCADADLAVITAGANQAPGETHLDLVEKNVKIFECIVKDMNSGDFGILLVATNP 127
QY 133 VDVLTYISYKASGFPPLSRVIGSGTVLDTARFKYILGHEHFKISSIDACVIGBGD--GVP 191
DB 128 VDILAHVTKVSGLPGRVIGSGTILDTARFYLSDYFEVDSNVHAYIMGEHGDTEFP 187
QY 192 VWSLTNIDGKMLRDYCEKANHIFDQAFHRIFFOTRDAAYDIIRKGYTSYGIAAGLLRI 251
DB 188 VWSHAQIGGVKLEHFINTA-AIEKEPDMQHLFEQTRDAAYHIINRKGATTYGIAMGLVRI 246
QY 252 VKAILEDGTSLTVSTV--GDYFVEQIATSVPTKLNKSGAHVAELSLDEKEITELMEKS 309
DB 247 TKAILDDENSILTVSALLEGQY-GISDVYIGVPAINKNGVRQIETLNLTPHQOQLEHS 305
QY 310 ASQIK 314

```

Db 306 ASILK 310

RESULT 4

LDH_CLOPE

ID - LDH_CLOPE STANDARD; PRT; 317 AA.

AC Q8XP62;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).

GN LDH OR CPE0103.

OS Clostridium perfringens.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1502;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;

RX MEDLINE=21664373; PubMed=11792842;

RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,

RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

RT "Complete genome sequence of *Clostridium perfringens*, an anaerobic

RT flesh-eater."

RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

CC -1- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.

CC -1- PATHWAY: Anaerobic glycolysis; final step.

CC -1- SUBUNIT: Homotetramer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.

CC

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CC

CC EMBL; AP003185; BAB79809.1; -.

DR HAMAP; MF_00488; -.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR00205; NAD_binding.
DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh_C; 1.
DR PRINTS; PR00086; LDHHRGNASE.
DR PROSITE; PS00064; L_LDH; 1.
DR Oxidoreductase; NAD; Glycolysis.
KW ACT SITE 178
FT ACT SITE 178 BY SIMILARITY.
SQ SEQUENCE 317 AA; 34522 MW; 88C862C0B2B3D951 CRC64;

Query Match 44.4%; Score 722; DB 1; Length 317;

Best Local Similarity 45.2%; Pred. No. 4e-46;

Matches 142; Conservative 69; Mismatches 97; Indels 6; Gaps 4;

QY 15 KTKVVVVGVSGSATATYLLSGIVSEIVLDVNVKDKAEGESMDLNHAAP--SNTSR 72

DB 5 KTKKSIIGAGFGVGTAFALMODGLASEIVIVDINKKAHAEAMDLAQGAAFVKSVDIK 64

QY 73 AGDYPDCAGAAIVITVTCGINKQKQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132

DB 65 SGDYATKDSDIVIITAGVCPKPGETRLDIINLNKLFQSFVEVVKYSPNSILLVSNP 124

QY 133 VDVLTYISYKASGFPPLSRVIGSGTVLDTARFKYILGHEHFKISSIDACVIGBGD--VP 191

DB 125 VDILTITVTKLSGFPKERVIGSGTVLDTARFKYILGHEHFKISSIDACVIGBGDSEIT 184

QY 192 VWSLTNIDGKMLRDYCEKANHIFDQAFHRIFFOTRDAAYDIIRKGYTSYGIAAGLLRI 251

DB 185 AWSLTNIAGANVEEYCKTVCANCDGSGFKKPELPEKYNAAEYIINSKGYTNAYALAVTRI 244

QY 135 VLTYSIKASGFPUSRVIGSGTDLTARFKYILGEHFKISDSIDACVIGEHGDG-VPVW 193
 Db 121 VLTFFLKESGMDPRKVFSGTDLTARLTIAHQHCGSPRSVHVTVIGEHGDSSEVPVW 180
 QY 194 SLTNIDGMKLRDYCEKANHIFPDQAFHRIEOTRDAAYDIKRGYTSYGIAGLLRIVK 253
 Db 181 SGAMIGIPQNMCOICQKC-DSKILENFAKTRAAAYEIERGATHYAIALAVADIVE 239
 QY 254 AILEDGTSTLTSTV-VGDYFGVEQIAISVPTKLNKGAHVAELSLDEKEIEMEKASQ 312
 Db 240 SIPDFEKRVLTLVYLEDYLGKVDLCISVPVTLGKHGVRIELNLENEEELAPRKASASI 299
 QY 313 IKSVEIHL 320
 Db 300 LKNAINEI 307

RESULT 6
 LDHP_BACPS STANDARD; PRT; 318 AA.
 AC P14561;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE L-lactate dehydrogenase P (EC 1.1.1.27) (L-LDH P).
 GN LDHP OR LCTA.
 OS Bacillus psychrosaccharolyticus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90241471; PubMed=2334516;
 RA Vckovski V., Schlatter D., Zuber H.;
 RT "Structure and function of L-lactate dehydrogenases from
 RT thermophilic, mesophilic and psychrophilic bacteria, IX.
 RT Identification, isolation and nucleotide sequence of two L-lactate
 RT dehydrogenase genes of the psychrophilic bacterium Bacillus
 RT psychrosaccharolyticus.";
 RL Biol. Chem. Hoppe-Seyler 368:1435-1446(1987).
 CC -1- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
 CC -1- PATHWAY: Anaerobic glycolysis; final step.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
 CC
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 CC
 CC EMBL; X55118; CAA38914.1;
 CC PIR; S08182; S08182.
 CC HSP; P00344; 1LDB.
 CC HAMAP; MF 00488; -; 1.
 CC InterPro; IPR001557; L_LDH.
 CC InterPro; IPR001236; ldh.
 CC Pfam; PF00056; ldh; 1.
 CC Pfam; PF02866; ldh.C; 1.
 CC PRINTS; PR00086; LLDHDEGNASE.
 CC PROSITE; PS00064; L_LDH; 1.
 CC Oxidoreductase; NAD; Glycolysis.
 CC ACT_SITE 179 179 BY SIMILARITY.

SQ SEQUENCE 318 AA; 35249 MW; F69165A3408E442A CRC64;
 Query Match 41.8%; Score 679; DB 1; Length 318;
 Best Local Similarity 45.8%; Pred. No. 5.9e-43;
 Matches 140; Conservative 60; Mismatches 98; Indels 8; Gaps 5;
 QY 18 KVVVVGSGVSATAYTLTSLGIVSEIVLIDVKNKKAEGESMDLNHA---APSNTRSRAG 74
 Db 8 RVALIGAGSVSSVAFALLNQSITEELVIIDLNENKAMDMLNKGKVPAPNPTKTWYG 67
 QY 75 DYPCAGAAIVITVCINGKNGKOTRMDLAANKANIMLEIIPNVAKPAPDILLIATNPVD 134
 Db 68 TYSCKDADIVICAGANQKPGSTRDLDELVEKNRIFPKGIVEEIMASGDFGIFLIATNPVD 127
 QY 135 VLTYSIKASGFPUSRVIGSGTDLTARFKYILGEHFKISDSIDACVIGEHGDG-VPVW 193
 Db 128 ILTYATWKSGLPKERIIGSTILDTGRFRFLGEYFDIAPANVHAYIIIEHGDTLPVW 187
 QY 194 SLTNIDGMKLRDYCEKANHIFPDQAFHRIEOTRDAAYDIKRGYTSYGIAGLLRIVK 253
 Db 188 SHADIGGISITELI-KRNPEYTMKLDLFINVRDAAYQIIIEKKGATFYGIAMGLARITK 246
 QY 254 AILEDGTSTLTSTV-GDYFGVEQIAISVPTKLNKGAHVAELSLDEKEIEMEKASAS 311
 Db 247 AILNENSVLTSTYLDGEY-GTVDYMGVPAVVRNNGRIEIVELTLENEEQOQFKHSAN 305
 QY 312 QIKSVI 317
 Db 306 VLKAIL 311

RESULT 7
 LDHX_BACPS STANDARD; PRT; 319 AA.
 AC P20619;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE L-lactate dehydrogenase X (EC 1.1.1.27) (L-LDH X).
 GN LDHX OR LCTB.
 OS Bacillus psychrosaccharolyticus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90241471; PubMed=2334516;
 RA Vckovski V., Schlatter D., Zuber H.;
 RT "Structure and function of L-lactate dehydrogenases from
 RT thermophilic, mesophilic and psychrophilic bacteria, IX.
 RT Identification, isolation and nucleotide sequence of two L-lactate
 RT dehydrogenase genes of the psychrophilic bacterium Bacillus
 RT psychrosaccharolyticus.";
 RL Biol. Chem. Hoppe-Seyler 371:103-110(1990).
 CC -1- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
 CC -1- PATHWAY: Anaerobic glycolysis; final step.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
 CC
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 CC
 CC EMBL; X55119; CAA38915.2;
 CC PIR; S08183; S08183.
 CC HSP; P00344; 1LDB.
 CC HAMAP; MF 00488; -; 1.
 CC InterPro; IPR001557; L_LDH.
 CC InterPro; IPR001236; ldh.
 CC

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DR InterPro: IPR000205; NAD_binding.
DR Pfam: PF00056; ldh; 1.
DR Pfam: PF02866; ldh_C; 1.
DR PRINTS: PR00086; LLDHGRGNASE.
DR PROSITE: PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis.
FT ACT SITE 179 179 BY SIMILARITY.
SQ SEQUENCE 319 AA; 35312 MW; B68509B5B138EB6 CRC64;

Query Match 41.0%; Score 673; DB 1; Length 319;
Best Local Similarity 46.1%; Pred. No. 1.6e-42;
Matches 141; Conservative 58; Mismatches 99; Indels 8; Gaps 5;

QY 18 KVVVGVGSGSATYATLLSGLVSEIVLIDVNDKKAEGSMDLNHA---APSNTRSRAG 74
DB 8 RVALIGAGSGSSYAFALLNQSITEELVIDVNDKKAEGSMDLNHA---APSNTRSRAG 67
QY 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 68 NYDDCKEADIVICAGANQKPGETRLDLVEKNLIPKSLVDQVWASGDFGFIATNPVD 127
QY 135 VLTYSYKAGFPPLSRVIGSGTVLDTARPKYLGEHFKISSDSIDACVIGEHGD-GVPVW 193
DB 128 ILTYATWKFSGLPKRVIGSGTILDSGRFLLGEYFDIAPANVHAHIIGEHGDTELPVW 187
QY 194 SLTNIDGKMLRDYCEKANHFIDQNAFHRIPEQTRDAAYDIIKKGYTSYGAAGLLRIVK 253
DB 188 SHADIGVVPVEELITR-NPEYKMDLDOLFVNVDRDAAYHIIKKGYTSYGAAGLLRIVK 246
QY 254 AILSDTGSTLTSTVSTV--GDYFGVQIAISVPTKLKSGAHQVAELSDEKEIELMEKSAS 311
DB 247 AILNNSVLTSTVSTVSTV--GDYFGVQIAISVPTKLKSGAHQVAELSDEKEIELMEKSAS 305
QY 312 QIKSVI 317
DB 306 VLKEIL 311

RESULT 8
LDH_BACCA
ID LDH_BACCA STANDARD; PRT; 317 AA.
AC P10655;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH.
OS Bacillus caldotenax.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1395;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88050101; PubMed=3675869;
RA Zuelli F., Weber H., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic
RT and mesophilic bacteria, VI. Nucleotide sequences of lactate
RT dehydrogenase genes from the thermophilic bacteria Bacillus
RT stearothermophilus, B. caldolyticus and B. caldotenax.";
RT Biol. Chem. Hoppe-Seyler 368:1167-1177(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87246643; PubMed=3297694;
RA Barstow D.A., Murphy J.P., Sharman A.F., Clarke A.R., Holbrook J.J.,
RA Atkinson T.;
RT "Amino acid sequence of the L-lactate dehydrogenase of Bacillus
RT caldotenax deduced from the nucleotide sequence of the cloned gene.";
RL Eur. J. Biochem. 165:581-586(1987).
CC -4- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
CC -1- PATHWAY: Anaerobic glycolysis; final step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
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-----
DR EMBL: M19395; AAA22565.1; -.
DR EMBL: M28336; AAA22563.1; -.
DR PIR: S00019; S00019.
DR HSSP: P00344; 1LDH.
DR HAMAP: MF 00488; -. 1.
DR InterPro: IPR001557; L_LDH.
DR InterPro: IPR001236; ldh.
DR InterPro: IPR000205; NAD_binding.
DR InterPro: IPR000594; ThiF_domain.
DR Pfam: PF00056; ldh; 1.
DR Pfam: PF02866; ldh_C; 1.
DR PRINTS: PR00086; LLDHGRGNASE.
DR PROSITE: PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis.
FT ACT SITE 179 179 BY SIMILARITY.
FT CONFLICT 51 51 L -> F (IN REF. 2).
FT CONFLICT 138 138 S -> G (IN REF. 2).
SQ SEQUENCE 317 AA; 34847 MW; 935C31DCLB0309A CRC64;

Query Match 41.0%; Score 667; DB 1; Length 317;
Best Local Similarity 45.6%; Pred. No. 4.5e-42;
Matches 139; Conservative 54; Mismatches 106; Indels 6; Gaps 4;

QY 18 KVVVGVGSGSATYATLLSGLVSEIVLIDVNDKKAEGSMDLNHA---APSNTRSRAG 74
DB 8 RVAVGTGTPVGASAFALNQSGIADEIVLIDANENKAEGSMDLNHA---APSNTRSRAG 67
QY 75 DYPDCAGAAIVIVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 68 DYDDCKEADIVICAGANQKPGETRLDLVDKNIAIFRSIVSWASGDFGFIATNPVD 127
QY 135 VLTYSYKAGFPPLSRVIGSGTVLDTARPKYLGEHFKISSDSIDACVIGEHGD-GVPVW 193
DB 128 ILTYATWKFSGLPKRVIGSGTILDTARFRLGIDYFAVAPTNVHAYIIGEHGDTELPVW 187
QY 194 SLTNIDGKMLRDYCEKANHFIDQNAFHRIPEQTRDAAYDIIKKGYTSYGAAGLLRIVK 253
DB 188 SQADIGVPIKLVESKGE-EAOKELERIFVNVDRDAAYQIIKKGYTSYGAAGLLRIVK 246
QY 254 AILSDTGSTLTSTVSTVGD-YFGVEQIAISVPTKLKSGAHQVAELSDEKEIELMEKSASQ 312
DB 247 AILHENAIIITVSAYLDGPGYGRDVVIGVPAVINRNGIREVIELDEEKKWFRSAAT 306
QY 313 IKSVI 317
DB 307 LKGVL 311

RESULT 9
LDH_BACCL
ID LDH_BACCL STANDARD; PRT; 317 AA.
AC Q59244;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH.
OS Bacillus caldolyticus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88050101; PubMed=3675869;
RA Zuelli F., Weber H., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic

```

RT and mesophilic bacteria, VI. Nucleotide sequences of lactate
 RT dehydrogenase genes from the thermophilic bacteria *Bacillus*
 RL *stearothermophilus*, *B. caldolyticus* and *B. caldotenax*.;
 Biol. Chem. Hoppe-Seyler 368:1167-1177(1987).
 CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
 CC -!- PATHWAY: Anaerobic glycolysis; final step.
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
 CC
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 CC
 CC EMBL; M19394; AAA22564.1; -;
 DR PIR; B29704; B29704.
 DR HSP; P00344; 1LDB.
 DR HAMAP; MF 00488; -; 1.
 DR InterPro; IPR001557; L_LDH.
 DR InterPro; IPR001236; ldh.
 DR InterPro; IPR00205; NAD_binding.
 DR InterPro; IPR000594; Thif_domain.
 DR Pfam; PF00056; ldh; 1.
 DR Pfam; PF02866; ldh C; 1.
 DR PRINTS; PR00086; LLDHDSGNASE.
 DR PROSITE; PS00064; L_LDH; 1.
 DR OXIDOREDUCTASE; NAD; Glycolysis.
 KW ACT SITE 179 179 BY SIMILARITY.
 FT ACT SITE 179 179 BY SIMILARITY.
 SQ SEQUENCE 317 AA; 34818 MW; 7A1D85428B0CD0E8 CRC64;
 Query Match 40.6%; Score 659; DB 1; Length 317;
 Best Local Similarity 45.2%; Pred. No. 1.8e-41;
 Matches 138; Conservative 53; Mismatches 108; Indels 6; Gaps 4;
 QY 18 KVVVGVGSGSATAYTLISGIVSEIVLIDVNDKKAEGESMDLNHA---APNTRSRAG 74
 DB 8 RVVVGTFGVGASVAFALMNGQIADEIVLIDANESKAIGDAMDNDHKGVPAPADLWHG 67
 QY 75 DYPDCAGAAIVVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
 DB 68 DYDCRDADLVICAGANQKPGETRLDLVDKNIAIFRSIVESVNASGQGLFLVATNPVD 127
 QY 135 VLTYSIKASGFPRLSRVIGSGTGLDTRFKYILGEHFKISDSIDACVIGEGD-GYPVW 193
 DB 128 ILTATWKFSGLPHERVIGSGTGLDTRFKYILGEHFVSVAPQNHYIIGEGDTPLPVW 187
 QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEQTRDAAYDIIRKGYTSYGIAGLLRIVK 253
 DB 188 SQADIGGVPIKLVESKGE-EAKELERIFVNVEDAAVQIIEKKGATYYGIAMGLARVTR 246
 QY 254 AILEDGSGTLTVSTVGD-YFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIEMKESASQ 312
 DB 247 ALLHNNAILTVSAYLDGPGYGERDVIYGVPAVINNRNGIREVETIELNDDEKNRPHHSAAT 306
 QY 313 IKSVI 317
 DB 307 LKSVL 311
 RESULT 10
 LDH_BACSD
 ID LDH_BACSD STANDARD; PRT; 310 AA.
 AC Q9K528;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
 GN LDH OR LCTE OR BH3937.
 OS *Bacillus halodurans*.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
 CC -!- PATHWAY: Anaerobic glycolysis; final step.
 CC -!- SUBUNIT: Homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
 CC
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 CC
 CC EMBL; AP001520; BAB07656.1; -;
 DR PIR; A84142; A84142.
 DR HSP; P00344; 2LDB.
 DR HAMAP; MF 00488; -; 1.
 DR InterPro; IPR001557; L_LDH.
 DR InterPro; IPR001236; ldh.
 DR InterPro; IPR00205; NAD_binding.
 DR InterPro; IPR000594; Thif_domain.
 DR Pfam; PF00056; ldh; 1.
 DR Pfam; PF02866; ldh C; 1.
 DR PRINTS; PR00086; LLDHDSGNASE.
 DR PROSITE; PS00064; L_LDH; 1.
 DR OXIDOREDUCTASE; NAD; Glycolysis; Complete proteome.
 KW ACT SITE 179 179 BY SIMILARITY.
 FT ACT SITE 179 179 BY SIMILARITY.
 SQ SEQUENCE 310 AA; 33406 MW; CCS16E904E57FE45 CRC64;
 Query Match 39.9%; Score 649; DB 1; Length 310;
 Best Local Similarity 45.2%; Pred. No. 9.3e-41;
 Matches 138; Conservative 53; Mismatches 100; Indels 14; Gaps 6;
 QY 18 KVVVGVGSGSATATLLISGIVSEIVLIDVNDKKAEGESMDLNHA---APNTRSRAG 74
 DB 8 KIVLVGTGAVGSSYAYALMNGQISDELILVDLNEEKAGDVLNHNISVYVSPFMEIKFG 67
 QY 75 DYPDCAGAAIVVTCGINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
 DB 68 SYEDCKDAALVVICAGAAKPGETRLDLVHKVNGVIFESIVGNMKSGFNGFIVATNPVD 127
 QY 135 VLTYSIKASGFPRLSRVIGSGTGLDTRFKYILGEHFKISDSIDACVIGEGD-GYPVW 193
 DB 128 ILAYATWKFSGLPKERVIGSGTGLDTRFKYILGEHSMNAAPTSHVGYIIGEGDSQLPVW 187
 QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEQTRDAAYDIIRKGYTSYGIAGLLRIVK 253
 DB 188 SSATIAGTPI-----APRLTDEKQ-QETAENVRDAAYKIIIEAKGATYYGIATGLARITR 240
 QY 254 AILEDGSGTLTVSTV--GDYFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIEMKESAS 311
 DB 241 ALLKNNVPLVGTLLGEN-GHDDVYIIGVPAIINREGVRQVVELSUNDEEKEFKARFVSVE 299
 QY 312 QIKSV 316
 DB 300 TLKDI 304
 RESULT 11
 LDH_BACST

LDH BACST STANDARD; PRT; 317 AA.
AC P00344;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (L-LDH).
GN LDH OR LCT.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OK NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106842; PubMed=3026926;
RA Barstow D.A., Clarke A.R., Chia W.N., Wigley D., Sharman A.F.,
RA Holbrook J.J., Atkinson T., Minton N.P.,
RT "Cloning, expression and complete nucleotide sequence of the Bacillus
RT stearothermophilus L-lactate dehydrogenase gene";
RL Gene 46:47-55(1986).
RN [2]
RP SEQUENCE.
RC STRAIN=NCIB 8924;
RX MEDLINE=84006440; PubMed=6352452;
RA Wirz B., Suter F., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic
RT and mesophilic bacteria. II) The primary structure of thermophilic
RT lactate dehydrogenase from Bacillus stearothermophilus.
RT Hydroxylamine-, o-iodobenzoic acid- and tryptic-fragments. The
RT complete amino-acid sequence.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:893-909(1983).
RN [3]
RP PARTIAL SEQUENCE.
RC STRAIN=NCIB 8924;
RX MEDLINE=84006439; PubMed=6618448;
RA Tratschin J.D., Wirz B., Frank G., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic
RT and mesophilic bacteria. II) The primary structure of thermophilic
RT lactate dehydrogenase from Bacillus stearothermophilus. Cyanogen
RT bromide fragments and partial sequence.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:879-892(1983).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92114070; PubMed=1731077;
RA Wigley D.B., Gamblin S.J., Turkenburg J.P., Dodson E.J., Piontek K.,
RA Muirhead H., Holbrook J.J.;
RT "Structure of a ternary complex of an allosteric lactate
RT dehydrogenase from Bacillus stearothermophilus at 2.5-A resolution.";
RL J. Mol. Biol. 223:317-335(1992).
CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
CC -!- PATHWAY: Anaerobic glycolysis; final step.
CC -!- SURUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
CC
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CC
CC EMBL; M14788; AAA22568.1; -;
DR EMBL; M19396; AAA22567.1; -;
DR EMBL; A06664; CAA00587.1; -;
DR PIR; A26053; DEBSLF.
DR PDB; 1LDH; 12-JUL-89.
DR PDB; 2LDH; 15-APR-90.
DR PDB; 1LDN; 31-JAN-94.
DR HAMAP; MF_00488; -; 1.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR000594; Thif_domain.

DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh.C; 1.
DR PRINTS; PS00086; LLDH; 1.
DR PROSITE; PS00084; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis; 3D-structure.
FT ACT_SITE 179 BY SIMILARITY.
FT CONFLICT 113 S -> H (IN REF. 3).
FT TURN 2 5
FT STRAND 8 12
FT HELIX 16 28
FT TURN 29 29
FT STRAND 33 37
FT HELIX 41 54
FT TURN 55 56
FT STRAND 63 66
FT HELIX 69 71
FT TURN 72 74
FT STRAND 77 80
FT TURN 88 90
FT HELIX 93 95
FT HELIX 96 113
FT TURN 114 114
FT STRAND 118 121
FT HELIX 126 137
FT TURN 138 138
FT HELIX 141 143
FT STRAND 144 146
FT TURN 148 149
FT HELIX 150 164
FT TURN 165 165
FT HELIX 168 170
FT STRAND 171 177
FT TURN 181 182
FT STRAND 184 192
FT TURN 193 194
FT STRAND 195 196
FT TURN 198 200
FT HELIX 202 204
FT TURN 205 207
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FT TURN 235 249
FT HELIX 250 251
FT STRAND 254 263
FT TURN 265 266
FT STRAND 269 280
FT TURN 281 282
FT STRAND 283 287
FT HELIX 294 313
SQ SEQUENCE 317 AA; 34863 MW; 4B146CF681C91046 CRC64;
Query Match 39.9%; Score 648; DB 1; Length 317;
Best Local Similarity 44.9%; Pred. No. 1.1e-40;
Matches 137; Conservative 51; Mismatches 111; Indels 6; Gaps 4;
Qy 18 KVVVGVGVSGATATVLLISGIVSEIVLIDVKNKRAEGESMDLHA---APSNTRSRAG 74
Db 8 RVVVGAGFGVGSVVFMNMQGIADIEVLIDANESKAIGDMDFNHGKVPAPVDFWHG 67
Qy 75 DYPDCAGAAIVTVTCINQKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
Db 68 DYDDCRDADLVWCAGANQKPGETRLDLDVKNKIAIFRSIVESVMSAGFQGLFLVATNPVD 127
Qy 135 VLTVISYKASGFPILSRVIGSGTVLDTARFKYIIGEHFKISSDSIDACVIGEGD-GVPVW 193
Db 128 ILTVATWFKSGLPHERVIGSGTILDTARFRLIGEVFSPVAPQNVHAYIIIGEGDTPLPW 187
Qy 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIEQTFRDAAYDIIKKGYTSYGIAAGLLRIVK 253
Db 188 SQAVIGWPIRKLVESKGE-EAOKDLERIFVNVDRDAAYQIIKKGATYYGIAMGLARVTR 246
Qy 254 AILEDGTSTLTSTVGD-YFGVEQIAISVPTKLNKSGAHQVAELSLDEKIELMEKASQ 312
Db 247 AILHNENAILTVSAYLDGLYGERDVVIGVPAVINRNGIRVIEIELNDDEKNRPHHSAAT 306

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medighe C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Furnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*";
RL Nature 390:249-256(1997).
RN (3)
RP SEQUENCE.
RX MEDLINE=87076052; PubMed=3098260;
RA Hediger M.A., Frank G., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from thermophilic
RT and mesophilic bacteria, IV. The primary structure of the mesophilic
RT lactate dehydrogenase from *Bacillus subtilis*.";
RL Biol. Chem. Hoppe-Seyler 367:891-903(1986).
CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
CC -!- PATHWAY: Anaerobic glycolysis; final step.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50453; BAA0939.1; ALT_INIT.
DR EMBL; Z99105; CAB12099.1; ALT_INIT.
DR PIR; B69649; E69649.
DR HSSP; P00344; 1LDB.
DR Subtilist; BG19003; ldh.
DR HAMAP; MF_00488; -; 1.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR00205; NAD_binding.
DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh; C; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR PROSITE; PS00064; L_LDH; 1.
DR Oxidoreductase; NAD; Glycolysis; Complete proteome.
FT ACT SITE 178 178 BY SIMILARITY.
FT CONFLICT 38 38 V -> L (IN REF. 3).
FT CONFLICT 51 51 P -> N (IN REF. 3).
FT CONFLICT 57 58 GL -> AP (IN REF. 3).
FT CONFLICT 120 120 V -> I (IN REF. 3).
FT CONFLICT 224 224 H -> T (IN REF. 3).
FT CONFLICT 315 318 MISSING (IN REF. 3).
SQ SEQUENCE 320 AA; 34786 MW; D2D9466A7329C95F CRC64;
Query Match 39.3%; Score 639; DB 1; Length 320;
Best Local Similarity 44.1%; Pred. No. 5.3e-40;
Matches 135; Conservative 56; Mismatches 109; Indels 6; Gaps 4;
QY 18 KVVVGVSGSAYAYTLLSGIVSEIVLIDVKNKDAEGSMIDLNHAAP---SNTRSRAG 74
DB 7 KVALIGAGFVSSYAFALINGITDELVIDVKNKAGMDVMDLPHGKATGLQVKTSYG 66
QY 75 DYPDCAAAIVITCGINKQNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134

Db 67 TYEDCKADADVICAGANQKPGTRELVEKNLKI FKGI VSEWASGFGDGIPLVATNPVD 126
QY 135 VLTIVSYKASGFPPLSVIGSGTGLDTRAFKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
Db 127 ILTYAKWKSGLPKERVIGSGTGLDSARFRMUSEYFGRAQPNVHAHII GEHGDTELPVW 186
QY 194 SLTNIDGMKLDYCEKANHFIDQNAFHRIPEQTRDAAYDIIRKGYTSYGAAGLLRIVK 253
Db 187 SHANVGVPVSELVEK-NDAYKQDELDQIVDDVKNAAHYHIEKKGATYYGVANSLARITK 245
QY 254 AILLEDGSLTIVSTVGD-VFGVEQIAISVPTKUNKSGAHQVAELSDLEKEIEMKESASQ 312
Db 246 AILHNENSILTVSTYLDGQYGVADVIVGPAVVNRGCIAGITELNLNKEKEQFLHSAGV 305
QY 313 IKSIVB 318
Db 306 LKNILK 311

RESULT 15

LDH2 LACLA
ID LDH2 LACLA STANDARD; PRT; 314 AA.
AC Q8CII4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-lactate dehydrogenase 2 (EC 1.1.1.27) (L-LDH 2).
GN LDHB OR LL0376.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Winkler P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
RT *lactis* sp. *lactis* IL1403";
RL Genome Res. 11:731-753(2001).
CC -!- CATALYTIC ACTIVITY: (S)-lactate + NAD(+) = pyruvate + NADH.
CC -!- PATHWAY: Anaerobic glycolysis; final step.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.
CC -----

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CC -----

EMBL; AE006274; AAK04474.1; --
DR PIR; H86671; H86671.
DR HSSP; P00344; 1LDB.
DR HAMAP; MF_00488; -; 1.
DR InterPro; IPR001557; L_LDH.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR00205; NAD_binding.
DR InterPro; IPR000594; Thif_domain.
DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh; C; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR PROSITE; PS00064; L_LDH; 1.
KW Oxidoreductase; NAD; Glycolysis; Complete proteome.
FT ACT SITE 178 178 BY SIMILARITY.
SQ SEQUENCE 314 AA; 34311 MW; 57289F439CF01DDA CRC64;

Query Match 38.6%; Score 627; DB 1; Length 314;
Best Local Similarity 43.9%; Pred. No. 3.9e-39;

	Matches 136;	Conservative 59;	Mismatches 107;	Indels 8;	Gaps 5;
Qy	18	KVVVGVSGSATATYLLLSGIVSEIVLIDVNDKKAEGESMDLNHA---	APSNTRSRAG	74	
Db	7	KVVWIGTGFVGTSAYSMINOGLVNLVLIIDVNDKKAEGEALDLDGVS	WQENVIVRAG	66	
Qy	75	DYPCAGAAIVIVTCGINQKNGOTRMDLAAKNANIMLEIIPNVA	KYAPDTILLIATNPVD	134	
Db	67	DYKCKNADI VVVVTAGVNDKQGRDLVNTNAKIMRSIVTQV	MDSGFDGIFVIASNPVD	126	
Qy	135	VLTIVSYKASGFPLSRVIGSGTVLDTARFKYILGEHFKISSDS	IDACVIGEHGDG-V	193	
Db	127	ILTVVAVWETSGLDQSRIVGTGTLLDTTFRKLATKLEIDPR	SVHGYIIEHGDSEVAVW	186	
Qy	194	SLTNIDGMKLRDYCEKANHIIDQNAFHRIPEQTRDAAYDII	KRKYTSYGTAGLLRIVK	253	
Db	187	SHTTVGGKPILEFIVKNKKIGVED-LSNLSNKNVNAAYEII	DKQATYIGIGMSTARIVK	245	
Qy	254	AILEDGTGSLTVSTV--GDYFQVQIAISVPTKLNKSGAHO	VAELSLDEKEIELMEKSAS	311	
Db	246	AILLNEQAILPVSAYLRGEY-GQGVFTGVPFSIVNQNGV	REIIEINIDAYEKKOFKSVS	304	
Qy	312	QIKSVIEHLE	321		
Db	305	QLKEVIESIK	314		

Search completed: July 25, 2003, 11:44:13
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2003, 11:41:32 ; Search time 98 Seconds
(without alignments)
850.520 Million cell updates/sec

Title: US-09-992-430B-22

Perfect score: 1625

Sequence: 1 MFODTKSQAVRTDAKTVKV.....ELMEKSASQIKSVIEHLEIN 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	753	46.3	315	2	Q8KQC4	Q8KQC4 clostridium
2	667.5	41.1	317	2	Q9S0N0	Q9S0N0 bacillus st
3	642.5	39.5	322	16	Q8FLV6	Q8FLV6 corynebacte
4	635	39.1	316	16	Q8CMZ0	Q8CMZ0 staphylococ
5	627	38.6	321	16	Q8ELF0	Q8ELF0 oceanobacil
6	592.5	36.5	325	2	P94885	P94885 lactococcus
7	586.5	36.1	325	2	P94886	P94886 lactococcus
8	583	35.9	346	10	O81272	O81272 solanum tub
9	582.5	35.8	347	10	Q96570	Q96570 lycopersico
10	581	35.8	332	13	Q9W7M7	Q9W7M7 xenopus lae
11	577.5	35.5	350	10	Q96569	Q96569 lycopersico
12	576.5	35.5	325	2	Q9R868	Q9R868 streptococ
13	576	35.4	329	16	Q8E5N4	Q8E5N4 streptococ
14	576	35.4	329	16	Q8DZY3	Q8DZY3 streptococ
15	574	35.3	332	13	Q9W5Z7	Q9W5Z7 xenopus lae
16	573	35.3	315	11	Q99K20	Q99K20 mus musculu

17	568.5	35.0	353	10	Q8LBDS	Q8LBDS arabidopsis
18	568	35.0	353	10	O23569	O23569 arabidopsis
19	567	34.9	353	10	O49191	O49191 arabidopsis
20	563	34.6	319	2	Q8GMW6	Q8GMW6 lactobacill
21	562.5	34.6	353	10	Q9ZRJ5	Q9ZRJ5 oryza sativ
22	561	34.5	332	11	Q9WVN8	Q9WVN8 cricetidae
23	556	34.2	338	5	O44340	O44340 styela plic
24	555.5	34.2	320	16	Q97DC6	Q97DC6 clostridium
25	554	34.1	323	2	Q8GMJ0	Q8GMJ0 lactobacill
26	553	34.0	333	13	O8UJQ5	O8UJQ5 columba liv
27	550.5	33.9	381	4	Q96LI2	Q96LI2 homo sapien
28	541	33.3	332	11	Q64483	Q64483 mus musculu
29	540	33.2	334	6	Q9MYV5	Q9MYV5 bos taurus
30	537	33.0	382	11	Q8EVP2	Q8EVP2 mus musculu
31	530	32.6	360	10	Q8LWZ6	Q8LWZ6 oryza sativ
32	511	31.4	311	16	O8Y6Z6	O8Y6Z6 listeria mo
33	506.5	31.2	303	1	Q9P9L2	Q9P9L2 halobacteri
34	503.5	31.0	318	2	Q9EVR0	Q9EVR0 selenomonas
35	498	30.6	311	16	Q92BI0	Q92BI0 listeria in
36	487	30.0	256	10	Q9SAN7	Q9SAN7 lycopersico
37	477.5	29.4	234	4	Q96LI9	Q96LI9 homo sapien
38	470	28.9	307	17	Q8PVJ7	Q8PVJ7 methanosarc
39	468.5	28.8	318	16	Q8D467	Q8D467 vibrio vuln
40	452.5	27.8	315	16	Q8EUG3	Q8EUG3 mycoplasma
41	448.5	27.6	317	17	Q8TWG5	Q8TWG5 methanopyru
42	446	27.4	309	17	Q8ZVB2	Q8ZVB2 pyrobaculum
43	437	26.9	307	17	Q8TSH7	Q8TSH7 methanosarc
44	435	26.8	312	16	O8EPE2	O8EPE2 oceanobacil
45	433.5	26.7	325	17	O26290	O26290 methanobact

ALIGNMENTS

RESULT 1

Q8KQC4 PRELIMINARY; PRT; 315 AA.

ID Q8KQC4

AC Q8KQC4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE L-lactate dehydrogenase.

OS Clostridium thermocellum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1515;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=27405;

RA Ozkan M., Lynd L.R., Ozcengiz G.;

RT "L-Lactate Dehydrogenase Gene of Clostridium thermocellum.";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE LDH FAMILY.

DR EMBL; AY098994; AAM29186.2; -

DR InterPro; IPR000345; CytC_heme_bind.

DR InterPro; IPR001236; ldh.

DR InterPro; IPR001557; L_LDH.

DR Pfam; PF00056; ldh; 1.

DR Pfam; PF02866; ldh C; 1.

DR PRINTS; PR00086; LLDHGRNASE.

DR PROSITE; PS00190; CYTOCHROME_C; 1.

DR PROSITE; PS00064; L_LDH; 1.

KW NAD; Oxidoreductase.

SQ SEQUENCE 315 AA; 34858 MW; 33BEC69CABD78AD1 CRC64;

Query Match 46.3%; Score 753; DB 2; Length 315;

Best Local Similarity 48.7%; Pred. No. 8.6e-49;

Matches 151; Conservative 63; Mismatches 88; Indels 8; Gaps 6;

QY 18 KVVVGVGVGGATATLLLSGIVSIVLIDVNVKAKGESMDLNHAAP--SNTRSRAGD 75

DB 9 KVTWVGFGVGGTATYTLMLSLGLISLIVLIDINAKKADGEVMDLNHGMPPFVRPEIYRGD 68

```

Qy 76 YPDCAGAAIVITCGINCKGOTMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVDV 135
Db 69 YKDCAGSDIVITITAGANKEGETRIDLVKRNTEVFNKIIINEIVYNNDCI-LVATNPVDI 127

Qy 136 LTYISYKASGFPPLSRVIGSGTVDLTARPKYILGBHFKISSDSIDACVIGEHGD-GVPVWS 194
Db 128 LTYITYKLSGFP-KQIIGSGTVDLTARPRYLLSEHVKVDARNVHAYIIGEHGDTVAAMS 186

Qy 195 LTNDIGMKLRDYCSKANHIFDQNAFHRIEOTRDAAYDIIKRGYTSYGIAGLLRIVKA 254
Db 187 LANIAGIPMDRYCDECHOCBEQISRNKIYESVKNAAYEIIIRKGCATYAYALAVRIVEA 246

Qy 255 ILEDTGSLTSTV--GDYFVGEQIAISVPTKLNKSGAHQVAELSLDEKTELMEKSASQ 312
Db 247 IVRNENSLTIVSSLEGQY-GLSDVCLSVPTIVGVNGIEELANVPFNDIEIQLLRKSGNT 305

Qy 313 IKSVIEHLEI 322
Db 306 HKEIKTLDI 315

RESULT 2
Q9SONO PRELIMINARY; PRT; 317 AA.
AC Q9SONO;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH).
GN LDH.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RA Nishiya Y.;
RT "Nucleotide sequence of the lactate dehydrogenase gene from Bacillus stearothermophilus ATCC12016.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; AB033627; BAA85589.1; -.
DR HSSP; P00344; ILDB.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR001557; L.LDH.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF00056; ldh; 1.
DR PRINTS; PR00866; ldh.C; 1.
DR PROSITE; PS00064; L.LDH; 1.
KW NAD; Oxidoreductase.
SQ SEQUENCE 317 AA; 34695 MW; 4E231DE1BE4F3246 CRC64;

Query Match 41.1%; Score 667.5; DB 2; Length 317;
Best Local Similarity 45.4%; Pred. No. 2.5e-42;
Matches 142; Conservative 56; Mismatches 108; Indels 7; Gaps 5;

Qy 10 VRTAKTVKVVVGVSGSATATYLLSGIVSEIVLIDVNDKKAEGESMDLNHA---AP 66
Db 1 MKNDGGT-RVVVIGTGFVGYAFALMNGQITDEIVLIDANESKAIGDAMDNLHGKVFAP 59

Qy 67 SNTRSAGDYPDCAGAAIVITCGINCKGOTMDLAANKANIMLEIIPNVAKYAPDTIL 126
Db 60 KPAVVRHGYSDDCHADLUVICAGANQKPGETRLDVLVDKNIAIFRSIVSVMASGFOGLF 119

Qy 127 LIATNPVDLTYISYKASGFPPLSRVIGSGTVDLTARPKYILGEHFKISSDSIDACVIGEH 186
Db 120 LVATNPVDLTYATWKPSGLPHERVIGSGTILDTARPRFLIGEYFVSAPQNVHAYIIEGH 179

Qy 187 GD-GVPVWSLTNDIGMKLRDYCEKANHIFDQNAFHRIEOTRDAAYDIIKRGYTSYGIAG 245
Db 180 GDTLPVWSQADIGGVPIRKLVE-AKGEQAKEELERIFTDVRDAAYQIIKKGATYYGIA 238

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Qy 246 AGLRIVKALIEDGTSTLTSTVGD-YFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIE 304
Db 239 MGLARVTRAILHNENAILTVSAYLDGPGYGERDVIYGVPAVNRNGIREVIEILNDDKEN 298

Qy 305 LMEKSASQIKSVI 317
Db 299 RFHSAATLKSVL 311

RESULT 3
Q8FLV6 PRELIMINARY; PRT; 322 AA.
AC Q8FLV6;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Putative L-lactate dehydrogenase.
GN CE2753;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Ueda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005223; BAC19563.1; -.
KW Complete proteome.
SQ SEQUENCE 322 AA; 35431 MW; CF00B95F46B2BA2C CRC64;

Query Match 39.5%; Score 642.5; DB 16; Length 322;
Best Local Similarity 45.6%; Pred. No. 2e-40;
Matches 141; Conservative 49; Mismatches 110; Indels 9; Gaps 5;

Qy 18 KVVVGVSGSATATYLLSGIVSEIVLIDVNDKKAEGESMDLNHA---APNTRSAG 74
Db 12 RVVLIGAGDVGVAAYALVNGQIADBLCIIDIDKLEGNVMDLSHGVMWAGKRTKVRKG 71

Qy 75 DYPCAGAAIVITCGINCKGOTMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
Db 72 TYSDECDANMVICAGAAQXPGETRLQVLDKXNVIMHTIVDEVMANGFDGLFLVATNPVD 131

Qy 135 VLTYSYKASGFPPLSRVIGSGTVDLTARPKYILGEHFKISSDSIDACVIGEHGD-GVPVW 193
Db 132 ILTYAVWKFSGLDHSRVIGSGTVDLTARPRYMLGELYDVSPKSTHAYIIGEHGDTLPVL 191

Qy 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIEOTRDAAYDIIKRGYTSYGIAGLLRIVK 253
Db 192 SSATIAGVMRKMLEDKPEL--EPRLKIFEDTRDAAYRIIDAKGSTSYGIGMLAKRITR 249

Qy 254 AILEDGTSTLTSTV--GDYFVGEQIAISVPTKLNKSGAHQVAELSLDEKEIEILMEKSAS 311
Db 250 AILNQDVALPVSAYLEGQY-GEEDIYIGTIPALIDRSIHVRVVEISDRMSRPFKSAQ 308

Qy 312 QIKSVIEHL 320
Db 309 TLRAIKDEI 317

RESULT 4
Q8CMZ0 PRELIMINARY; PRT; 316 AA.
AC Q8CMZ0;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase.
GN SE2145.
OS Staphylococcus epidermidis.

```

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 QX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A5016751; AAO05787.1; -;
 KW Complete proteome.
 SQ SEQUENCE 316 AA; 34101 MW; D11D4B1958125A23 CRC64;
 Query Match 39.1%; Score 635; DB 16; Length 316;
 Best Local Similarity 43.1%; Pred. No. 7e-40;
 Matches 137; Conservative 57; Mismatches 100; Indels 24; Gaps 6;
 QY 18 KVVVGSGVSGATATLLSGIVSEIVLDVKNKKAEGSMDLNHA--PSNTRSRAG 74
 DB 7 KVLVGGSGVSGYAFAMVTQGIADFEVLIIDAKDKVEADVKNLHNGALYSSSPVTVKAG 66
 QY 75 DYPDCAGAAIVIVTCGINQKQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
 DB 67 EYEDCKADLVITAGAPKCPGTRQLQVKNKSIIVTSVMSDGFDFGLIAPNPVD 126
 QY 135 VLTIYSYKASGFLSRVIGSGTVLTARPKYLGBHFKISSDSIACVIGHGSG-VPVW 193
 DB 127 ILTRYVKEVTGLPAERVIGSGTVLDSARFRLYISKELGVTSSSVHASIIGHGSGSELA 186
 QY 194 SLTNDIGMKLRDyce-----KANHI PQDQAFHRIFEQTRDAAYDIIRKGYTSYGIAA 246
 DB 187 SQANVGGSIVDTLKEETGSDAKAN-----EYINTRDAAYDIIRKGYTSYGIAL 237
 QY 247 GLLRIVKAILEDTGSTLTVST--VGYFVGEQIAISVPTKLNKSGAHQVAELSDEKIEL 305
 DB 238 ALLRISKALLNNENSLTVSSQLNGQYGFNDVGLPLTINQNGANKYIETPLNDNELQL 297
 QY 306 MEKSGASQIKSV---TEHL 320
 DB 298 LEKSVKTLDTYDSIKHL 315
 RESULT 5
 Q8ELF0 PRELIMINARY; PRT; 321 AA.
 ID Q8ELF0
 AC Q8ELF0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE L-lactate dehydrogenase (EC 1.1.1.27).
 GN OB3279.
 OS Oceanobacillus iheyensis.
 OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
 QX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
 RX MEDLINE=22220767; PubMed=12235376;
 RA Takami H., Takaki Y., Uchiyama I.;
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935 (2002).
 DR EMBL; AP004604; BAC15235.1; -;
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 321 AA; 35252 MW; B02F605CF2B5E00E CRC64;
 Query Match 38.6%; Score 627; DB 16; Length 321;
 Best Local Similarity 43.4%; Pred. No. 2.9e-39;
 Matches 139; Conservative 54; Mismatches 113; Indels 14; Gaps 6;
 QY 5 TKSOAVRTDAKTVKVVVGSGVSGATAYTLLSGIVSEIVLDVKNKKAEGSMDLNHA 64
 DB 3 TSOQAVN-----RVLLTGGGSGVSYAFALMNGQVTEELAIIDLDADKALGDVMDLNHG 56

Germain V., Ricard B.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.
CC -1- PATHWAY: ANAEROBIC GLYCOLYSIS; FINAL STEP.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; Y08887; CAA70100.1; -.
DR EMBL; Y10602; CAA71611.1; -.
DR HSSP; P00339; 9LDT.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR001557; L_LDH.
DR Pfam; PF00056; ldh; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR PROSITE; PS00064; L_LDH; 1.
KW NAD; Oxidoreductase.
FT ACT SITE 210 210 BY SIMILARITY.
SQ SEQUENCE 350 AA; 37708 MW; 3957C1D4F804D70F CRC64;

Query Match 35.5%; Score 577.5; DB 10; Length 350;
Best Local Similarity 36.9%; Pred. No. 1.8e-35;
Matches 115; Conservative 74; Mismatches 116; Indels 7; Gaps 4;

QY 18 KVVVGVGSGSATATYLLLSGIVSEIVLIDVNVKKAEGESMDLNHAA--PSNTRSR 74
DB 39 KISVIGVNGVMAIAQTILITQDLDELALVDKSKLRGEMDLQHAFAFLPRKTHASI 98
QY 75 DYPDCAGAAIVITCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 99 DYSVTAGSLCIVTAGARQNPESRLNLRQNWALFRSLIIPLVKYSETILLVVSNPVD 158
QY 135 VLTYISYKASGFPPLSRVIGSGTLDTRFVKYILGEHPKISSDISDACVIGEHGD-GVPVW 193
DB 159 VLTYVAVKLSGFPANRVIGSGTNLDSRRFELIADHLVDNAQDVQAYIVGEGSSVALW 218
QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEOTRDAAYDIIRKGYTSYGAAGLLRIVK 253
DB 219 SGISVSGVPLSFRLERQIALEKTELEKHQEVHSAVEVLSLKYTSWAIGYSVANLAR 278
QY 254 AILEDGTSTLTSTVSG-DYFVGE--QIATSVPTKLKNSGAHOVAELSDEKEIEMKSA 310
DB 279 TILRQRRHPVSLAKGFGIDGGVFLSLPAQLGRSGVLGVTVNHLTDSIEQLRNSA 338
QY 311 SQIKSVIEHLEI 322
DB 339 KTILEVQSQGI 350

RESULT 12
Q9R868 PRELIMINARY; PRT; 325 AA.
AC Q9R868
AC Q9R868
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH) (Fragment).
GN LDH.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
RN NCBI_TaxID=1313;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=7785;
RX MEDLINE=99240355; PubMed=10223925;
RA Pan X.S., Fisher M.L.;
RT "Streptococcus pneumoniae DNA gyrase and topoisomerase IV:
RT overexpression, purification, and differential inhibition by
RT fluoroquinolones."
RL Antimicrob. Agents Chemother. 43:1129-1136(1999).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; AJ005815; CAA06714.1; -.
DR HSSP; P00344; 2LDB.
DR InterPro; IPR001236; ldh.

RA Germain V., Ricard B.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.
CC -1- PATHWAY: ANAEROBIC GLYCOLYSIS; FINAL STEP.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; Y08887; CAA70100.1; -.
DR EMBL; Y10602; CAA71611.1; -.
DR HSSP; P00339; 9LDT.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR001557; L_LDH.
DR Pfam; PF00056; ldh; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR PROSITE; PS00064; L_LDH; 1.
KW NAD; Oxidoreductase.
FT ACT SITE 210 210 BY SIMILARITY.
SQ SEQUENCE 350 AA; 37708 MW; 3957C1D4F804D70F CRC64;

Query Match 35.5%; Score 577.5; DB 10; Length 350;
Best Local Similarity 36.9%; Pred. No. 1.8e-35;
Matches 115; Conservative 74; Mismatches 116; Indels 7; Gaps 4;

QY 18 KVVVGVGSGSATATYLLLSGIVSEIVLIDVNVKKAEGESMDLNHAA--PSNTRSR 74
DB 39 KISVIGVNGVMAIAQTILITQDLDELALVDKSKLRGEMDLQHAFAFLPRKTHASI 98
QY 75 DYPDCAGAAIVITCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 99 DYSVTAGSLCIVTAGARQNPESRLNLRQNWALFRSLIIPLVKYSETILLVVSNPVD 158
QY 135 VLTYISYKASGFPPLSRVIGSGTLDTRFVKYILGEHPKISSDISDACVIGEHGD-GVPVW 193
DB 159 VLTYVAVKLSGFPANRVIGSGTNLDSRRFELIADHLVDNAQDVQAYIVGEGSSVALW 218
QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEOTRDAAYDIIRKGYTSYGAAGLLRIVK 253
DB 219 SGISVSGVPLSFRLERQIALEKTELEKHQEVHSAVEVLSLKYTSWAIGYSVANLAR 278
QY 254 AILEDGTSTLTSTVSG-DYFVGE--QIATSVPTKLKNSGAHOVAELSDEKEIEMKSA 310
DB 279 TILRQRRHPVSLAKGFGIDGGVFLSLPAQLGRSGVLGVTVNHLTDSIEQLRNSA 338
QY 311 SQIKSVIEHLEI 322
DB 339 KTILEVQSQGI 350

RESULT 12
Q9R868 PRELIMINARY; PRT; 325 AA.
AC Q9R868
AC Q9R868
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH) (Fragment).
GN LDH.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
RN NCBI_TaxID=1313;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=7785;
RX MEDLINE=99240355; PubMed=10223925;
RA Pan X.S., Fisher M.L.;
RT "Streptococcus pneumoniae DNA gyrase and topoisomerase IV:
RT overexpression, purification, and differential inhibition by
RT fluoroquinolones."
RL Antimicrob. Agents Chemother. 43:1129-1136(1999).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; AJ005815; CAA06714.1; -.
DR HSSP; P00344; 2LDB.
DR InterPro; IPR001236; ldh.

RA Germain V., Ricard B.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.
CC -1- PATHWAY: ANAEROBIC GLYCOLYSIS; FINAL STEP.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; Y08887; CAA70100.1; -.
DR EMBL; Y10602; CAA71611.1; -.
DR HSSP; P00339; 9LDT.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR001557; L_LDH.
DR Pfam; PF00056; ldh; 1.
DR PRINTS; PR00086; LLDHGRNASE.
DR PROSITE; PS00064; L_LDH; 1.
KW NAD; Oxidoreductase.
FT ACT SITE 210 210 BY SIMILARITY.
SQ SEQUENCE 350 AA; 37708 MW; 3957C1D4F804D70F CRC64;

Query Match 35.5%; Score 577.5; DB 10; Length 350;
Best Local Similarity 36.9%; Pred. No. 1.8e-35;
Matches 115; Conservative 74; Mismatches 116; Indels 7; Gaps 4;

QY 18 KVVVGVGSGSATATYLLLSGIVSEIVLIDVNVKKAEGESMDLNHAA--PSNTRSR 74
DB 39 KISVIGVNGVMAIAQTILITQDLDELALVDKSKLRGEMDLQHAFAFLPRKTHASI 98
QY 75 DYPDCAGAAIVITCGINOKNGQTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPVD 134
DB 99 DYSVTAGSLCIVTAGARQNPESRLNLRQNWALFRSLIIPLVKYSETILLVVSNPVD 158
QY 135 VLTYISYKASGFPPLSRVIGSGTLDTRFVKYILGEHPKISSDISDACVIGEHGD-GVPVW 193
DB 159 VLTYVAVKLSGFPANRVIGSGTNLDSRRFELIADHLVDNAQDVQAYIVGEGSSVALW 218
QY 194 SLTNIDGMKLRDYCEKANHIFDQNAFHRIPEOTRDAAYDIIRKGYTSYGAAGLLRIVK 253
DB 219 SGISVSGVPLSFRLERQIALEKTELEKHQEVHSAVEVLSLKYTSWAIGYSVANLAR 278
QY 254 AILEDGTSTLTSTVSG-DYFVGE--QIATSVPTKLKNSGAHOVAELSDEKEIEMKSA 310
DB 279 TILRQRRHPVSLAKGFGIDGGVFLSLPAQLGRSGVLGVTVNHLTDSIEQLRNSA 338
QY 311 SQIKSVIEHLEI 322
DB 339 KTILEVQSQGI 350

RESULT 12
Q9R868 PRELIMINARY; PRT; 325 AA.
AC Q9R868
AC Q9R868
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH) (Fragment).
GN LDH.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
RN NCBI_TaxID=1313;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=7785;
RX MEDLINE=99240355; PubMed=10223925;
RA Pan X.S., Fisher M.L.;
RT "Streptococcus pneumoniae DNA gyrase and topoisomerase IV:
RT overexpression, purification, and differential inhibition by
RT fluoroquinolones."
RL Antimicrob. Agents Chemother. 43:1129-1136(1999).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; AJ005815; CAA06714.1; -.
DR HSSP; P00344; 2LDB.
DR InterPro; IPR001236; ldh.

RA Germain V., Ricard B.;
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(

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Qy 74 GDYPCAGAAIVITVCGINQKNGOTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPV 133
Db 69 ATYADCADADLWITAGAPQKPGETRLDLVKGKLNAINKSIVTQVVEGFGIFLVAANPV 128
Qy 134 DVLTYISYKASGFFPLSRVIGSGTGLDTRAFKYLGEHFHFKISSDSIDACVIGEHGOG-VPV 192
Db 129 DVLTYSTWKFSGFPKERVIGSGTGLDTRAFKYLGEHFHFKISSDSIDACVIGEHGOG-VPV 188
Qy 193 WSLTNIDGMKLRDYCEKANHFIDQNAFHRIEQTDRDAAYDIIKRGKGYTSYGIAAGLLRIV 252
Db 189 WSHANVAGVQLEQWLOE-NRDIDEGGLVDLFIISVRDAAYSIIINKGATYYGIAVALARIT 247
Qy 253 KAILLEDGTSTLTVSTV--GDYFGVEQIAISVPTKLKNGSGAHQVAELSLDEKEIEMLEKSA 310
Db 248 KAILDDENAVLPLSVYQEGYQGVKDFVIGQPAIVGAHGIVRPVPNIPLNDAELQKMQASA 307
Qy 311 SQIKSVIE 318
Db 308 EQLKDIID 315

RESULT 14
Q8DZY3 PRELIMINARY; PRT; 329 AA.
AC Q8DZY3;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase.
GN LDH OR SAG0959.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547;
RA Tettelin H., Masiugnani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radu D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014235; AAM99843.1; -.
DR TIGR; SAG0959; -.
KW Complete proteome.
SQ SEQUENCE 329 AA; 35418 MW; 999D4BD9D9160B9A CRC64;

Query Match 35.4%; Score 576; DB 16; Length 329;
Best Local Similarity 41.2%; Pred. No. 2.1e-35;
Matches 127; Conservative 58; Mismatches 115; Indels 8; Gaps 5;

Qy 18 KVVVGVGSGSATATYLLISGIVSEIVLIDVKN--DKAEGESMDLNHAA--PSNTRSR 73
Db 9 KVLIVGDAVGSYAFALVNOGIAQELGIIIEIPALFDKAVGDAEDLSHALAFTSPKIIYA 68
Qy 74 GDYPCAGAAIVITVCGINQKNGOTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNPV 133
Db 69 ATYADCADADLWITAGAPQKPGETRLDLVKGKLNAINKSIVTQVVEGFGIFLVAANPV 128
Qy 134 DVLTYISYKASGFFPLSRVIGSGTGLDTRAFKYLGEHFHFKISSDSIDACVIGEHGOG-VPV 192
Db 129 DVLTYSTWKFSGFPKERVIGSGTGLDTRAFKYLGEHFHFKISSDSIDACVIGEHGOG-VPV 188
Qy 193 WSLTNIDGMKLRDYCEKANHFIDQNAFHRIEQTDRDAAYDIIKRGKGYTSYGIAAGLLRIV 252
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Db 189 WSHANVAGVQLEQWLOE-NRDIDEGGLVDLFIISVRDAAYSIIINKGATYYGIAVALARIT 247
Qy 253 KAILLEDGTSTLTVSTV--GDYFGVEQIAISVPTKLKNGSGAHQVAELSLDEKEIEMLEKSA 310
Db 248 KAILDDENAVLPLSVYQEGYQGVKDFVIGQPAIVGAHGIVRPVPNIPLNDAELQKMQASA 307
Qy 311 SQIKSVIE 318
Db 308 EQLKDIID 315

RESULT 15
Q9W5Z7 PRELIMINARY; PRT; 332 AA.
AC Q9W5Z7;
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE L-lactate dehydrogenase M chain (EC 1.1.1.27) (LDH).
GN LDH-A OR LDHA2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Mannen H., Li S.S.-L.;
RT "Molecular evidence for a clade of turtles.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Tsai S.C.-M., Li J.Y., Mannen H., Li S.S.-L.;
RT "Molecular evolution of vertebrate lactate dehydrogenase isozymes by
RT gene duplication.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.
CC -I- PATHWAY: ANAEROBIC GLYCOLYSIS; FINAL STEP.
CC -I- SIMILARITY: BELONGS TO THE LDH FAMILY.
DR EMBL; AF072582; AAD41639.1; -.
DR EMBL; AF070953; AAD40731.1; -.
DR HSSP; P00339; 9LDT.
DR InterPro; IPR001236; ldh.
DR InterPro; IPR001557; L_LDH.
DR Pfam; PF00056; ldh; 1.
DR Pfam; PF02866; ldh; C; 1.
DR PRINTS; PR00086; LLDHGRGNASE.
DR PROSITE; PS00064; L_LDH; 1.
KW Glycolysis; NAD; Oxidoreductase.
SQ SEQUENCE 332 AA; 36472 MW; C293E0B4B79441B3 CRC64;

Query Match 35.3%; Score 574; DB 13; Length 332;
Best Local Similarity 39.4%; Pred. No. 3e-35;
Matches 123; Conservative 65; Mismatches 114; Indels 10; Gaps 5;

Qy 18 KVVVGVGSGSATATYLLISGIVSEIVLIDVKN--DKAEGESMDLNHAA--PSNTRSR 72
Db 22 KVTIVGVGAVGMAICAVSLQKDLADELALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGK 81
Qy 73 AGDYPDCAGAAIVITVCGINQKNGOTRMDLAANKANIMLEIIPNVAKYAPDTILLIATNP 132
Db 82 --DYSVTANSKLVVVTAGARQEGESRLNLVQRNVAIFRILINIVKYSFNTLLIVSNP 139
Qy 133 DVLTYISYKASGFFPLSRVIGSGTGLDTRAFKYLGEHFHFKISSDSIDACVIGEHGOG-VPV 191
Db 140 VDILTIVAWKISGFPKRVNIGSGNLSARFRLMGQKFGIHTQSGCHGWIGEHGDSVP 199
Qy 192 WSLTNIDGMKLRDYCEKANHFIDQNAFHRIEQTDRDAAYDIIKRGKGYTSYGIAAGLLRIV 251
Db 200 WSGVNVAGVSLKTLHPDIDGSDADKENWKEVHVQVDSAYEVLKLGKGYTSWAIGLSVADL 259
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Qy 252 VKAILEDGTSTLTVST-VGDYFGV-EQIAISVPTKLNKSGAHQVAELSLSLDEKEIETELMEKS 309
Db 260 SESILKNLRRVHPISITMVKMGIVNNDVFLSPCVLGNLGITDVNNMTLKADEEDRLRKS 319
Qy 310 ASQIKSVIEHLE 321
Db 320 ADTLWAIQKEIQ 331

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Search completed: July 25, 2003, 11:45:59.
Job time : 100 secs